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OM nucleic - nucleic search, using sw model

Run on: September 1, 2005, 00:42:12 ; Search time 529 seconds  
(without alignments)  
10306.378 Million cell updates/sec

Title: US-09-964-277-20  
Perfect score: 3332  
Sequence: 1 gagagaagagagataata.....ataaagatgaactggtttc 3332

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2950	88.5	3544	4	US-09-816-494-1
2	1660	49.8	1998	4	US-09-816-494-3
3	294.6	8.8	333	4	US-09-513-999C-2877
4	247	7.4	279	4	US-09-016-434-91
5	225.2	6.8	2377	4	US-09-920-668-3
6	223.6	6.7	2351	4	US-09-949-016-3250
7	187.8	5.6	378	4	US-09-513-999C-3684
8	109.6	3.3	1830	4	US-09-557-921-1
9	95	2.9	2283	4	US-09-949-016-4617
10	95	2.9	2303	4	US-09-922-146-3
11	94.6	2.8	1208	4	US-09-023-655-347
12	90.2	2.7	2109	4	US-09-016-434-1135
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14	90.2	2.7	2475	4	US-09-949-016-2615
15	89.2	2.7	13782	4	US-09-949-016-14992
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17	85.6	2.6	1619	4	US-09-702-705-801
18	85.6	2.6	1619	4	US-09-736-457-801
19	85.6	2.6	1619	4	US-09-614-124B-801
20	85.6	2.6	1619	4	US-09-671-325-801
21	85.6	2.6	1619	4	US-09-589-184-801
22	85.6	2.6	1619	4	US-09-658-824-801
23	85.6	2.6	1619	4	US-09-702-705-804
24	85.6	2.6	4637	4	US-09-736-457-804
25	85.6	2.6	4637	4	US-09-614-124B-804
26	85.6	2.6	4637	4	US-09-671-325-804
27	85.6	2.6	4637	4	US-09-589-184-804

28	85.6	2.6	4637	4	US-09-658-824-804	Sequence 804, App
29	84	2.5	1238	2	US-08-530-290-11	Sequence 11, Appl
30	84	2.5	1238	4	US-09-702-705-803	Sequence 803, App
31	84	2.5	1238	4	US-09-736-457-803	Sequence 803, App
32	84	2.5	1238	4	US-09-614-124B-803	Sequence 803, App
33	84	2.5	1238	4	US-09-671-325-803	Sequence 803, App
34	84	2.5	1238	4	US-09-589-184-803	Sequence 803, App
35	84	2.5	1238	4	US-09-702-705-825	Sequence 825, App
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37	84	2.5	2064	4	US-09-614-124B-825	Sequence 825, App
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39	84	2.5	2064	4	US-09-589-184-825	Sequence 825, App
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41	84	2.5	2109	4	US-09-702-705-826	Sequence 826, App
42	84	2.5	2109	4	US-09-736-457-826	Sequence 826, App
43	84	2.5	2109	4	US-09-614-124B-826	Sequence 826, App
44	84	2.5	2109	4	US-09-671-325-826	Sequence 826, App
45	84	2.5	2109	4	US-09-589-184-826	Sequence 826, App

ALIGNMENTS

RESULT 1  
US-09-816-494-1  
; Sequence 1, Application US/09816494  
; Patent No. 6664089  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel A.  
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY  
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR  
; FILE REFERENCE: 10448-030002  
; CURRENT APPLICATION NUMBER: US/09/816,494  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/191,858  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3544  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (589)...(2583)  
US-09-816-494-1

Query Match	88.5%	Score	2950;	DB	4;	Length	3544;
Best Local Similarity	95.0%	Pred. No.	0;				
Matches	3135;	Conservative	0;	Mismatches	0;	Indels	165;
Gaps	2;						
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Db	224	GCTTTTCAGTCCAGTGTAAAGCTGTTGGAGCGGGAGCAAGGTAAGAAATGATGTAATG	283				
QY	257	CGTGTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTTCCAGTCATCTCTTTATGA	316				
Db	284	CGTGTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTTTCCAGTCATCTCTTTATGA	343				
QY	317	ATCAAAATGTAGGGGCTGCTTTGTGGAAGGTCCTTTGCAAGAGCACATCAACGGGAAA	376				
Db	344	ATCAAAATGTAGGGGCTGCTTTGTGGAAGGTCCTTTGCAAGAGCACATCAACGGGAAA	403				
QY	377	GAGAAAGACATTCATCTTTGGGGCTCTTGCTGAAATGGGTTTAACTCTCTTTTGGC	436				
Db	404	GAGAAAGACATTCATCTTTGGGGCTCTTGCTGAAATGGGTTTAACTCTCTTTTGGC	463				
QY	437	AGTCACACACAGCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC	496				
Db	464	AGTCACACACAGCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGC	523				
QY	497	ACACACACATTCATCATCGTGGCAATTAAGAGAGGAGTGGGAAAAGAGGACTTATTG	556				

Db	524	ACACCACATTACATCATCGTGGCAAAATTAAGAGGAGGCTGGGAAAGAGACATTATTG	583
QY	557	TTGTCAATGCCCATGAGATGATGGAACTCAAAATTTACTGAGAGGTTGGTGGCTCTGC	616
Db	584	TTGTCAATGCCCATGAGATGATGGAACTCAAAATTTACTGAGAGGTTGGTGGCTCTGC	643
QY	617	TGGAAGTGGAAACGGAAAGTGTCTTAATTTGATAGCCGGCCATTTTGGGAATACAATA	676
Db	644	TGGAAGTGGAAACGGAAAGTGTCTTAATTTGATAGCCGGCCATTTTGGGAATACAATA	703
QY	677	CATCCACATTTTGAAGCCATTAAATATCAAACTGTCTCAAGCTTATGAAGCGAAGGTTGC	736
Db	704	CATCCACATTTTGAAGCCATTAAATATCAAACTGTCTCAAGCTTATGAAGCGAAGGTTGC	763
QY	737	AACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTTACGCGAAACAAATAGGTTGACA	796
Db	764	AACAGACAAAGTGTAAATACAGAGCTCATCCAGCATTTACGCGAAACAAATAGGTTGACA	823
QY	797	TTGATTTGAGTCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCT	856
Db	824	TTGATTTGAGTCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCT	883
QY	857	CTTCAGACTGTTTTCTCACTGACTTCTGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC	916
Db	884	CTTCAGACTGTTTTCTCACTGACTTCTGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC	943
QY	917	ACCTGCTTGC-----	926
Db	944	ACCTGCTTGCAGGTGGTTTGTGAGTTCTCTCGTTGTTTCCCTGGCTCTCTGGAAGGAA	1003
QY	927	-----	926
Db	1004	AATCCACTGATGCCCTACCTGCAATTTCTACGCTTTGCTTACCTGTGTCACAACTGGGC	1063
QY	927	-----AGGAGC	932
Db	1064	CAACCCGAATTTTCCCAATCTTTATCTTGGCTGCCAGCGAGATGTCCTCAACAGGAGC	1123
QY	933	TGATGAGCAGAAATGGGATTTAGTGTAAATGCGCAAGAAATACCTGTCCAAAGCCGTG	992
Db	1124	TGATGAGCAGAAATGGGATTTAGTGTAAATGCGCAAGAAATACCTGTCCAAAGCCGTG	1183
QY	993	ACTTTATCCCGAGTCTCATTTCTCGCGTGCCTGTGAAATCACAGCTTTTCTGAGAAAA	1052
Db	1184	ACTTTATCCCGAGTCTCATTTCTCGCGTGCCTGTGAAATCACAGCTTTTCTGAGAAAA	1243
QY	1053	TTTTGCGGTGGTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCTCCAAATGGAT	1112
Db	1244	TTTTGCGGTGGTGGACAAATCAGTAGATTTTCATTGAGAAAGCAAAAGCCTCCAAATGGAT	1303
QY	1113	GTGTTCTAGTGCACTGTTAGCTGGGATCTCCGGCTCCGCCACCATCGCTATCGCCTACA	1172
Db	1304	GTGTTCTAGTGCACTGTTAGCTGGGATCTCCGGCTCCGCCACCATCGCTATCGCCTACA	1363
QY	1173	TCAATGAAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC	1232
Db	1364	TCAATGAAGAGGATGGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC	1423
QY	1233	CTACTATATCTCCAAATCTCAATTTTCTGGGGCAACTCTCTGGACTATGAGAGAAAGATTA	1292
Db	1424	CTACTATATCTCCAAATCTCAATTTTCTGGGGCAACTCTCTGGACTATGAGAGAAAGATTA	1483
QY	1293	AGAACAGACTGTGAGCATCAGGCGCCAAAGAGCAAACTCAAGCTGTGCACTCTGGAGAGC	1352
Db	1484	AGAACAGACTGTGAGCATCAGGCGCCAAAGAGCAAACTCAAGCTGTGCACTCTGGAGAGC	1543
QY	1353	CAAAATGAACCTGTCCCTGTCTCAGAGGTTGGACAGAAAGCGAGAGCGCCCTCAGTC	1412
Db	1544	CAAAATGAACCTGTCCCTGTCTCAGAGGTTGGACAGAAAGCGAGAGCGCCCTCAGTC	1603
QY	1413	CACCTGTGCCGACTCTGCTACCTCAGAGGCGAGCAGCAAAAGGCCGTGCACTCCGCCA	1472
Db	1604	CACCTGTGCCGACTCTGCTACCTCAGAGGCGAGCAGCAAAAGGCCGTGCACTCCGCCA	1663
QY	1473	CGTGCCCGAGCGTCCCGAGCGTCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG	1532
Db	1664	CGTGCCCGAGCGTCCCGAGCGTCAGCCGTCGCTGTTAGAGGACAGCCCGCTGGTACAGG	1723
QY	1533	CGCTCAGTGGGCTGCACCTGTCCGAGACAGGCTGGGAAGACAGCAATAAGCTCAAGCGTT	1592
Db	1724	CGCTCAGTGGGCTGCACCTGTCCGAGACAGGCTGGGAAGACAGCAATAAGCTCAAGCGTT	1783
QY	1593	CCTTCTCTCTCGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG	1652
Db	1784	CCTTCTCTCTCGATATCAAAATCAGTTTCATATTCAGCCAGCATGGCAGCATCCTTACATG	1843
QY	1653	GCTTCTCTCTCATCAGAAAGCTTTGGAAATCTCAAAACCTTCCACTACTCTGGATGGGA	1712
Db	1844	GCTTCTCTCTCATCAGAAAGCTTTGGAAATCTCAAAACCTTCCACTACTCTGGATGGGA	1903
QY	1713	CCAAACAGCTATGCGAGTTCTCCCTGTTCAGGAACTATCGAGCAGACTCCCGAAAAACA	1772
Db	1904	CCAAACAGCTATGCGAGTTCTCCCTGTTCAGGAACTATCGAGCAGACTCCCGAAAAACA	1963
QY	1773	GTCTCTGATTAAGAGGAAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAGACA	1832
Db	1964	GTCTCTGATTAAGAGGAAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAGACA	2023
QY	1833	GCCAGAGCAAGCGATTGCATTTGGTTCAGAAACAGGAGCTGGCACCGCCAGAGGTCCC	1892
Db	2024	GCCAGAGCAAGCGATTGCATTTGGTTCAGAAACAGGAGCTGGCACCGCCAGAGGTCCC	2083
QY	1893	TTTTATCTTCCACTCGAAGTGGAGCGTGGAGGACAAATTAACCAACCAAGCTTCTTTT	1952
Db	2084	TTTTATCTTCCACTCGAAGTGGAGCGTGGAGGACAAATTAACCAACCAAGCTTCTTTT	2143
QY	1953	TCGGCTTTTCCACGAGCAGACACTCAGCAAGTCTGTGGCTGGGCTTAAAGGCT	2012
Db	2144	TCGGCTTTTCCACGAGCAGACACTCAGCAAGTCTGTGGCTGGGCTTAAAGGCT	2203
QY	2013	GGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACGAGCAGCTGGTATT	2072
Db	2204	GGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACGAGCAGCTGGTATT	2263
QY	2073	TTGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGAGGAGCAGTGCAGTT	2132
Db	2264	TTGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTACGAGGAGCAGTGCAGTT	2323
QY	2133	ACTCTGCCCTACAGCTGCAGCAGCTGCCCACTTTCGGGAGACCAAGTCTATTCTGTGGCA	2192
Db	2324	ACTCTGCCCTACAGCTGCAGCAGCTGCCCACTTTCGGGAGACCAAGTCTATTCTGTGGCA	2383
QY	2193	GGCGCAGAACCCAGTGCACAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGCCCT	2252
Db	2384	GGCGCAGAACCCAGTGCACAGAGCTGACTCGCGCGGAGCTGGCATGAGAGAGCCCT	2443
QY	2253	TTGAAAAGCAGTTTAAACCCAGAAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTGAG	2312
Db	2444	TTGAAAAGCAGTTTAAACCCAGAAAGCTGCCAAATGGAAATTTGGAGAGAGCATCATGTGAG	2503
QY	2313	AGAACAGCTCAGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCTAGCTTTTCGGGAGCA	2372
Db	2504	AGAACAGCTCAGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCTAGCTTTTCGGGAGCA	2563
QY	2373	TGGAAATCATTTGAGGTCCTCTGAGAGAAAGACACTTCTGACTTCTATAGACAAATTTTT	2432
Db	2564	TGGAAATCATTTGAGGTCCTCTGAGAGAAAGACACTTCTGACTTCTATAGACAAATTTTT	2623
QY	2433	TTTTCTTTTCAAAAAAATTTCCCTGTAAATCTGAAATATATATATATGTACATACATAT	2492
Db	2624	TTTTCTTTTCAAAAAAATTTCCCTGTAAATCTGAAATATATATATATGTACATACATAT	2683
QY	2493	ATTTTTTGGAAAATGGAGCTATGGTGTAAAGCAACAGGTGGATCAACCCAGTTGTACTTC	2552
Db	2684	ATTTTTTGGAAAATGGAGCTATGGTGTAAAGCAACAGGTGGATCAACCCAGTTGTACTTC	2743

QY	2553	TCTTAACATCTGCTATTTGAGAGATCAGCTAATCTCTCTCAACAAAAATGGAAGGCGAG	2612
DB	2744	TCTTAACATCTGCTATTTGAGAGATCAGCTAATCTCTCTCAACAAAAATGGAAGGCGAG	2803
QY	2613	ATGCTAGAAATCCCTCTAGACGAGGAAACCAATTTTATTCAGTGAATTTACACATCTCT	2672
DB	2804	ATGCTAGAAATCCCTCTAGACGAGGAAACCAATTTTATTCAGTGAATTTACACATCTCT	2863
QY	2673	TGTTCTTAAAGCAAGTGTCTTTGGTCTTGAGGACAAAAATCCCTACCAATTTTCCAC	2732
DB	2864	TGTTCTTAAAGCAAGTGTCTTTGGTCTTGAGGACAAAAATCCCTACCAATTTT-CAC	2922
QY	2733	GTGTGCTACTAAGAGATCTCAAAATATAGTCTTTTGTCCGGACCCCTTCCATAGTACACCT	2792
DB	2923	GTGTGCTACTAAGAGATCTCAAAATATAGTCTTTTGTCCGGACCCCTTCCATAGTACACCT	2982
QY	2793	TAGCGCTGAGACTGAGCCAGTGTGGGGTCAAGTAGGTAGACCTGTATTAGGACAGAGCC	2852
DB	2983	TAGCGCTGAGACTGAGCCAGTGTGGGGTCAAGTAGGTAGACCTGTATTAGGACAGAGCC	3042
QY	2853	TAGTGTAAATCCAGAGAAATGATCCTATCCAAAGCTGATTCACAAAACCCAGCTCACCC	2912
DB	3043	TAGTGTAAATCCAGAGAAATGATCCTATCCAAAGCTGATTCACAAAACCCAGCTCACCC	3102
QY	2913	TGACGCCGAGGACACGAGCATCACTCTGTGCGACGACCAATTAGGGGCTTGGCCAAGG	2972
DB	3103	TGACGCCGAGGACACGAGCATCACTCTGTGCGACGACCAATTAGGGGCTTGGCCAAGG	3162
QY	2973	TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTGGGGCTTTGACCACTACCAT	3032
DB	3163	TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTGGGGCTTTGACCACTACCAT	3222
QY	3033	ATCTGTAGCCATTTTCTAGGCAATTTGTAATAGGTAGGTAGTACCTACACATTTTCAGA	3092
DB	3223	ATCTGTAGCCATTTTCTAGGCAATTTGTAATAGGTAGGTAGTACCTACACATTTTCAGA	3282
QY	3093	CCAAATTCAAACTCTCTATGACAAAAATCCCGTGGGCTAGATGGAGATAAATTTTTTTT	3152
DB	3283	CCAAATTCAAACTCTCTATGACAAAAATCCCGTGGGCTAGATGGAGATAAATTTTTTTT	3342
QY	3153	CTTCTCAGCTTTTATGAAGAAAGGAAACTGTCTAGGATTCAGCTGAACCAACGAGAAC	3212
DB	3343	CTTCTCAGCTTTTATGAAGAAAGGAAACTGTCTAGGATTCAGCTGAACCAACGAGAAC	3402
QY	3213	TGGCAACATCAGATTTAACTAAGTGTGGAGGCTTAAACAGTCTACCTCCCTCTTTGTA	3272
DB	3403	TGGCAACATCAGATTTAACTAAGTGTGGAGGCTTAAACAGTCTACCTCCCTCTTTGTA	3462
QY	3273	AATCAAGAAATTTTAAATGGATTTGTCAAATCCCTTAAATAAAGATGAATTTGGTTTC	3332
DB	3463	AATCAAGAAATTTTAAATGGATTTGTCAAATCCCTTAAATAAAGATGAATTTGGTTTC	3522

RESULT 2  
 US-09-816-494-3  
 ; Sequence 3, Application us/09816494  
 ; Patent No. 6664089  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meyers, Rachel A.  
 ; TITLE OF INVENTION: 38692 And 21117, NOVEL DUAL SPECIFICITY  
 ; PHOSPHATASE MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: 10448-030002  
 ; CURRENT APPLICATION NUMBER: US/09/816,494  
 ; CURRENT FILING DATE: 2001-03-23  
 ; PRIOR FILING DATE: 2000-03-24  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1998  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-816-494-3

		Query Match	49.8%;	Score 1660;	DB 4;	Length 1998;		
		Best Local Similarity	91.8%;	Pred. No. 0;				
		Matches 1834;	Conservative	0;	Mismatches	0;	Indels 164;	Gaps 1;
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DB	1	ATGGCCCATGATGATGATGGAACTCAAAATTTGTTACTGAGAGGTTGGTGGCTCTGCTGAA	60					
QY	622	AGTGAACCGGAAAAAGTCTGCTAAATTTGATAGCGGGCCATTTGTGGAATACAATACATCC	681					
DB	61	AGTGAACCGGAAAAAGTCTGCTAAATTTGATAGCGGGCCATTTGTGGAATACAATACATCC	120					
QY	682	CACATTTTGAAGCAATTAATCAACCTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG	741					
DB	121	CACATTTTGAAGCAATTAATCAACCTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG	180					
QY	742	GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTCAT	801					
DB	181	GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGGTTGACATTCAT	240					
QY	802	TGCACTCAGAAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCCTCTCTCTCTCA	861					
DB	241	TGCACTCAGAAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTTGCCCTCTCTCTCTCA	300					
QY	862	GACTGTTTCTCAGTGTACTTTCTGGGTAAACTGGGAGAGAGCTTCAACTCTCTTCACTG	921					
DB	301	GACTGTTTCTCAGTGTACTTTCTGGGTAAACTGGGAGAGAGCTTCAACTCTCTTCACTG	360					
QY	922	CTTGC-----	926					
DB	361	CTTGCAGGTGGGTTTGTCTGAGTCTCTCTGTTGTTTCCCTGGCCTCTGTGAAGGAAATCC	420					
QY	927	-----	926					
DB	421	ACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACTATGGGCCAAC	480					
QY	927	-----	937					
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QY	938	CAGCAAGATGGGATGTTGTTATGTGTTAAATGTCAGCAATACCTGTCCAAAGCTGACTTT	997					
DB	541	CAGCAAGATGGGATGTTGTTATGTGTTAAATGTCAGCAATACCTGTCCAAAGCTGACTTT	600					
QY	998	ATCCCGGAGTCTCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1057					
DB	601	ATCCCGGAGTCTCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660					
QY	1058	CCGTGGTTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCCTCCAAATGGATGTT	1117					
DB	661	CCGTGGTTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCCCTCCAAATGGATGTT	720					
QY	1118	CTAGTGCACTGTTTGTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCCGCTACATCATG	1177					
DB	721	CTAGTGCACTGTTTGTAGTGGGATCTCCCGCTCCGCCACCATCGCTATCCGCTACATCATG	780					
QY	1178	AAGGAGTGGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTACT	1237					
DB	781	AAGGAGTGGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTACT	840					
QY	1238	ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAAAGAAATTAAGAAC	1297					
DB	841	ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAAAGAAATTAAGAAC	900					
QY	1298	CAGACTGGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGCACTGAGAAAGCCAAAT	1357					
DB	901	CAGACTGGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGCACTGAGAAAGCCAAAT	960					
QY	1358	GAACCTGCTCCCTGCTCTCAGAGGTTGGACAGAAAGGAGACGCCCTCTAGTCCACCC	1417					
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QY 1418 TGTGCGGACTGTGCTACCTCAGAGGAGCAGACGAGCAAGGCGCGTGCATCCCGCAGCGTG 1477
Db 1021 TGTGCGGACTGTGCTACCTCAGAGGAGCAGACGAGCAAGGCGCGTGCATCCCGCAGCGTG 1080
QY 1478 CCAGCGGTCCCGAGCGGTGCGCTGCTGTAGAGGACAGCGCGCTGTGTACAGCGGCTC 1537
Db 1081 CCAGCGGTCCCGAGCGGTGCGCTGCTGTAGAGGACAGCGCGCTGTGTACAGCGGCTC 1140
QY 1538 AGTGGGCTGCACCTGTCCGAGACAGGCTGGAGAGCAGCAATAAGCTCAAGCGTTCCTTC 1597
Db 1141 AGTGGGCTGCACCTGTCCGAGACAGGCTGGAGAGCAGCAATAAGCTCAAGCGTTCCTTC 1200
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Db 1381 GATAGGAGGAGGAGCAGCATCCCGAGAGCTGCCAGCCGAGCGCTTCAGACAGCCAG 1440
QY 1838 AGCAACCGATTTGATTCGGTTCAGAAACAGCAGCAGTGGCCGCGCCAGAGTCCCTTTTA 1897
Db 1441 AGCAACCGATTTGATTCGGTTCAGAAACAGCAGCAGTGGCCGCGCCAGAGTCCCTTTTA 1500
QY 1898 TCTCCAATGATGAGTGGAGCGTGGAGGAGCAATTAACAACAGCTTCCTTTTCGGC 1957
Db 1501 TCTCCAATGATGAGTGGAGCGTGGAGGAGCAATTAACAACAGCTTCCTTTTCGGC 1560
QY 1958 CTTTCCACAGCCAGCAGCAGCTCAGAGTCTGCTGGCGTGGCGCTTAAGGGCTGGCAC 2017
Db 1561 CTTTCCACAGCCAGCAGCAGCTCAGAGTCTGCTGGCGTGGCGCTTAAGGGCTGGCAC 1620
QY 2018 TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATTTTGC 2077
Db 1621 TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTATTTTGC 1680
QY 2078 ACAGAGTCTCACTTCTACTCTGCTCAGCCATCTACGAGGAGTCCAGTACTCT 2137
Db 1681 ACAGAGTCTCACTTCTACTCTGCTCAGCCATCTACGAGGAGTCCAGTACTCT 1740
QY 2138 GCCTACAGCTGAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGCAGGGG 2197
Db 1741 GCCTACAGCTGAGCCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGCAGGGG 1800
QY 2198 CAGAGCCAAAGTGACAGAGTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTTGA 2257
Db 1801 CAGAGCCAAAGTGACAGAGTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTTGA 1860
QY 2258 AAGCAGTTTAAACGAGAGAGTCCCAATGGAAATTTGGAGAGAGCATATGTGAGAGAC 2317
Db 1861 AAGCAGTTTAAACGAGAGAGTCCCAATGGAAATTTGGAGAGAGCATATGTGAGAGAC 1920
QY 2318 AGGTACGGGAGAGCTGGGGAAGTGGGAGTCACTAGCTTTTTCGGGAGCATGGAA 2377
Db 1921 AGGTACGGGAGAGCTGGGGAAGTGGGAGTCACTAGCTTTTTCGGGAGCATGGAA 2377
QY 2378 ATCATTGAGGTCTCCTGA 2395
Db 1981 ATCATTGAGGTCTCCTGA 1998

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RESULT 3  
 US-09-513-999C-2877  
 ; Sequence 2877, Application US/09513999C  
 ; Patent No. 6783961

```

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2877
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..333
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17
; OTHER INFORMATION: h=a or c or t
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: y=c or t
; NAME/KEY: misc_feature
; LOCATION: 19
; OTHER INFORMATION: k=g or t
; NAME/KEY: misc_feature
; LOCATION: 36
; OTHER INFORMATION: n=a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: 58
; OTHER INFORMATION: r=a or g
; NAME/KEY: misc_feature
; LOCATION: 237
; OTHER INFORMATION: w=a or t
; NAME/KEY: UNSURE
; LOCATION: 37
; OTHER INFORMATION: Xaa=His or Gln
; US-09-513-999C-2877

```

Query Match 8.8%; Score 294.6; DB 4; Length 333;  
 Best Local Similarity 97.3%; Pred. No. 2.1e-82;  
 Matches 326; Conservative 5; Mismatches 0; Indels 4; Gaps 3;

```

QY 595 ACTGAGAGTGTGGTGGCTCTGCTGGAAGTGGAAAGG-AAAAAGTGTGCTAATTGATAG 653
Db 1 ACTGAGAGTGTGGTGGHY--KCTGGAAGTGGAAAGGAAAAAGTGTGCTAATTGATAR 58
QY 654 CCGGCCATTTTGTGAATA-CAATACATCCACATTTTGGAAAGCCATTAATATCAACTGCT 712
Db 59 CCGGCCATTTTGTGAATAACCAATACATCCACATTTTGGAAAGCCATTAATATCAACTGCT 118
QY 713 CAAGCTTATGAAGCGAAGTGTGCAAGGACAAAGTGTTAATACAGAGCTCATCCAGC 772
Db 119 CAAGCTTATGAAGCGAAGTGTGCAAGGAGTTGCAACAGGACAAAGTGTTAATACAGAGCTCATCCAGC 178
QY 773 ATTACGCGAAACATAAAGTGTGACATTGATTGAGTCAGAGAGTGTAGTTACGATCAAA 832
Db 179 ATTACGCGAAACATAAAGTGTGACATTGATTGAGTCAGAGAGTGTAGTTACGATCAAA 238
QY 833 GCTCCCAAGATGTTGCCTCTCTCTTCAGACTGTTTTCTCACTGCTACTTCTGGGTAAAC 892
Db 239 GCTCCCAAGATGTTGCCTCTCTCTTCAGACTGTTTTCTCACTGCTACTTCTGGGTAAAC 298

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QY 893 TGGAGAGAGCTTCAACTCTGTTCACTGCTTGA 927  
 Db 299 TGGAGAGAGCTTCAACTCTGTTCACTGCTTGA 333

RESULT 4  
 US-09-016-434-91  
 ; Sequence 91, Application US/09016434  
 ; Patent No. 650938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HEREMITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 91:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 279 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: LUNGFET03  
 ; CLONE: 1234795  
 ; US-09-016-434-91

Query Match 7.4%; Score 247; DB 4; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 538 GGGAAAAGAGACTTATTGTTGTCATGCCCATGAGATGATTGGAACCTCAAATGTTACT 597  
 Db 1 GGGAAAAGAGACTTATTGTTGTCATGCCCATGAGATGATTGGAACCTCAAATGTTACT 60  
 QY 598 GAGAGTTGGTCTGCTGGAAAGTGGAAACGAAAGTGTCTTAATGATAGCCG 657  
 Db 61 GAGAGTTGGTCTGCTGGAAAGTGGAAACGAAAGTGTCTTAATGATAGCCG 120  
 QY 658 CCATTTGGAATACATATCCACATTTTGAAGCCATTATATCAACTGCTCCAAG 717  
 Db 121 CCATTTGGAATACATATCCACATTTTGAAGCCATTATATCAACTGCTCCAAG 180  
 QY 718 CTTATGAAGCGAAGTTGCAACAGGAGCAAAAGTGTAAATACAGAGCTCATCCAGATTCA 777  
 Db 181 CTTATGAAGCGAAGTTGCAACAGGAGCAAAAGTGTAAATACAGAGCTCATCCAGATTCA 240

QY 778 GCGAAAC 784  
 Db 241 GCGAAAC 247

RESULT 5  
 US-09-920-668-3  
 ; Sequence 3, Application US/09920668  
 ; Patent No. 6482644  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lex M. Cowbert  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION  
 ; FILE REFERENCE: RTS-0246  
 ; CURRENT APPLICATION NUMBER: US/09/920,668  
 ; CURRENT FILING DATE: 2001-08-01  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 3  
 ; LENGTH: 2377  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (135)... (2012)  
 ; US-09-920-668-3

Query Match 6.8%; Score 225.2; DB 4; Length 2377;  
 Best Local Similarity 60.6%; Pred. No. 9.9e-60;  
 Matches 418; Conservative 0; Mismatches 248; Indels 24; Gaps 2;  
 QY 927 AGGAGCTGATGAGCAGAGATGGGATTGTTATGTGTAAATCCAGCAATACCTGTCCAA 986  
 Db 670 AGGATCTGATGAGCAGCAAAATGAATAGCTACGTCTCAAGCCAGCAACTCTGTGCCCA 729  
 QY 987 AGCTGACTTTATCCCGAGTCTCATTTCTCGGTGTGCTGTGATGACAGCTTTTGTG 1046  
 Db 730 AGCTGACTTCTATCGCGAGAGCCGTTTCATCGGGTCCCATCAACGACAACTACTGTG 789  
 QY 1047 AGAAAATTTTGGCTGGTGGCAAAATCAGTAGATTTTCAATGAGAAAGCAAGCCTCCA 1106  
 Db 790 AAAAATCTGCTGCTGGCTGGCAAACTCATGAGTTTCAATGAGAAAGCAAGCCTCCA 849  
 QY 1107 ATGGATGTGTTCTAGTGCACTGTTTATGTTGGATCTCCCGCTCCGCAACATGCTATCG 1166  
 Db 850 GCTGCCAAGTCTATCGTCCACTGTCTGGTGGCATCTCCCGCTGCGCAACATCGCCATCG 909  
 QY 1167 CTTACATCATGAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAA 1226  
 Db 910 CTTACATCATGAGACCATGGGCATGTCTCCGACGACGCCTACAGGTTCTGTAAGGACA 969  
 QY 1227 AAAGACCTACTATATCTCCAAATTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAAGA 1286  
 Db 970 GGCGCCCTGCTCATCTCGCCCAACTTCACTTCTGGGCCAGCTCTGCTGGAGTAGAGCGCA 1029  
 QY 1287 AGATTAAAGAACAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTGCTGACCTGG 1346  
 Db 1030 CGCTGAGCTGTGGCGCCCTCGAGGGCGACCCCGGCCACCCCTCAGGAGC-CCGG 1086  
 QY 1347 AGAAGCCAAATGAACCTGTCCTGTGTCTCAGAGGGTGGACAGAAAGGAGAGACGCCCC 1406  
 Db 1087 AGCTCCGCCAGTCTCTCGCGCGGGCCCGCTGCGAGGGTGGCCACCACTACCTACCTAG 1146  
 QY 1407 TCAGTCCACCTGTGCGGACTCTGCTACCTCAGAGGCACGAGGACAAAGCCGTCATC 1466  
 Db 1147 AGAGCCCTGCCACAGGGAATGCGGCTGCGAGGAGGGG-CCCCCCCCCCCC----- 1185  
 QY 1467 CGCCAGCTGCCAGCTGCCAGGTCGCCAGGTCGAGCCGCTGCTGTTAGAGGACAGCCGCTGG 1526  
 Db 1186 GCCTGAGCGGGCGGGAGCCCCCGCGCCCCCGCGCCCGGCGGACGAGCGCACTGC 1245  
 QY 1527 TACAGCGCTCAGTGGGCTGCACCTGTCCGACAGAGGCTGGAGAGCAGCAATAAGCTCA 1586

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Db      1246  AGCAGGGCGCTGGCGGCGCTGACCTCTCTCTGGAGCCGGCTGCGAGGACACTAACCGGCTCA 1305

Qy      1587  AGCGTTCCTTCTCTCTGGATATCAATCAG 1616
          ||||| ||||| ||||| |||||
Db      1306  AGCGTCTCTTCTCTCCCTGGACATCAAGTCTG 1335

RESULT 6
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

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Db      1165  -----AGCGGGGGGGAGCCCCCGCGCCCCCCCACGCCCGGGGACAGGCGCACTGC 1219
Qy      1527  TACAGGCGCTCAGTGGGCTGCACCTGTCTCCGCAGACAGAGGCTGGGAAGACAGCAATAAGCTCA 1586
Db      1220  AGCAGGGCTGCGGGCGCTGCACCTCTCTCGGACCGCTGCAGGACACTAACCGCCTCA 1279
Qy      1587  AGCTTCTCTTCTCTCTGGATATCAAAATCAG 1616
Db      1280  AGGCTCCTTCTCCCTGGACATCAAGTCTG 1309

RESULT 7
US-09-513-999C-3684/c
; Sequence 3684, Application US/09513999C
; Patent NO. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3684
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..377
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 164
; OTHER INFORMATION: k=g or t
US-09-513-999C-3684

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; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-921-1

Query Match      3.3%; Score 109.6; DB 4; Length 1830;
Best Local Similarity 61.0%; Pred. No. 3.6e-23;
Matches 178; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 1006 GTCCTCATTTTCCTCGCTGTCCTGTGAATCAGACGCTTTTGTGAGAAATTTTCCCGTGGTT 1065
DB 1187 GTTCACTACAAGCGCTCCAGCCACTGACAGCAACAGCAGACCTCGCGCAGTACTT 1246
QY 1066 GGACAAATCAGTAGATTTCAATTTGAGAAACAAAGCCTCCAATGGATGTTTCTAGTGA 1125
DB 1247 TGAAGAGGCTTTGAGTTCAATTTGAGGAAGCTCACCAGTGTGGGAAGGCTTCTCATCA 1306
QY 1126 CTGTTTAGCTGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGGAT 1185
DB 1307 CTGCCAGGCTGGGGTCTCCCGCTCCGCCACCATCGCTATCGCTTACTTGATGAAGCAC 1366
QY 1186 GGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTTACTATCTCC 1245
DB 1367 TCGATGACCATGACTGATGCTTATTAATTTGTCAAGCAACGACCAATATCTCC 1426
QY 1246 AAACCTTCAATTTTCTGGGCAACTCTCGGACTATGAGAAAGATTAAGAAC 1297
DB 1427 AAACCTTAACTTATCGGCGAGTTGCTAGAGTTGAGGAAGACCTTAACAAC 1478

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RESULT 9
US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4617
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4617

```

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Query Match      2.9%; Score 95; DB 4; Length 2283;
Best Local Similarity 58.8%; Pred. No. 1.8e-18;
Matches 164; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTCTCGCTGTCCTGTGAATGACAGCTTTTGTGAGAAATTTTCCCGTGG 1063
DB 858 GACTTTCACTACAAGCAGATCCCATCTCCGACCATCTGGAGCAGAACCTGTGCGGTT 917
QY 1064 TTGACAAATCAGTAGATTTCAATTTGAGAAACAAAGCCTCCAATGGATGTTTCTAGTG 1123
DB 918 TTTCCGAGGCGCATTTGAGTTCAATTTGAGGSCCTTGTCCAGAACCTGCGGGTCTCGTC 977
QY 1124 CACTGTTAGCTGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAG 1183

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DB 978 CACTGCTTGGCGGGGTGAGCCGTTCTGTCTACCGTCACTGTGGCTTACTCATCGAAG 1037
QY 1184 ATGCACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTTACTATCT 1243
DB 1038 CTCACCTCTCTCTCAACGATGCTATGACCTGTGCAAGAGGAAGTCTTAACATCTCC 1097
QY 1244 CCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAG 1282
DB 1098 CCCAACTTCAACTTTCATGGGCGAGTTGCTGGACTTTGAG 1136

RESULT 10
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseart
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)...(1268)
US-09-922-146-3

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```

Query Match      2.9%; Score 95; DB 4; Length 2303;
Best Local Similarity 58.8%; Pred. No. 1.8e-18;
Matches 164; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTCTCGCTGTCCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCCGTG 1063
DB 858 GACTTTCACTACAAGCAGATCCCATCTCCGACCATCTGGAGCCAGAACCTGTGCGGTT 917
QY 1064 TTGCAAAATCAGTAGATTTCAATTTGAGAAACAAAGCCTCCAATGGATGTTTCTAGTG 1123
DB 918 TTTCCGAGGCGCATTTGAGTTCAATTTGATGAGGCTTGTCCAGAACCTGCGGGTCTCGTC 977
QY 1124 CACTGTTAGCTGGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAG 1183
DB 978 CACTGCTTGGCGGGGTGAGCGCTTCTGTCAACGCTCACTGTGCGCTTACTCATGAGAAG 1037
QY 1184 ATGCACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTTACTATCT 1243
DB 1038 CTCACCTCTCTCTCAACGATGCTTATGACCTGTGTCAGAGGAAGAGTCTTAACATCTCC 1097
QY 1244 CCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAG 1282
DB 1098 CCCAACTTCAACTTTCATGGGCGAGTTGCTGGACTTTGAG 1136

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RESULT 11
US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA

```

```
/
/
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016.434
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0002 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1135:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2109 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g1418933
/ US-09-016-434-1135

Query Match 2.7%; Score 90.2; DB 4; Length 2109;
Best Local Similarity 57.1%; Pred. No. 5.6e-17;
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTTCCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTGCCTGG 1063
DB 1105 GAGTTTAATAACAGCAATCCCATCTCGATCACTGGAGCCAAACCTGTCCAGTTT 1164
QY 1064 TTGACAAATCAGTAGATTTTCATTGAGAAAGCAAGCCTCAATGGATGTGTTCTAGTG 1123
DB 1165 TTCCCTGAGGCCATTTCTTTTCATAGATGAAGCCGGGCAAGAACTGTGGTGTCTTGGA 1224
QY 1124 CACTGTTTAGCTGGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGG 1183
DB 1225 CATTGCTTGGCTGGCAATAGCCGCTCAGTCACTGTGACTGTGGCTTACTTTATGCAGAAG 1284
QY 1184 ATGACATGCTTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGAACTACTATATCT 1243
DB 1285 CTCATCTGTCGATGAACGATGCCTATGACATTTGTCAAAATGAAAAATCCAAACATAATCC 1344
QY 1244 CAAACCTTCAATTTTCTGGGCCAACTCCTGGACTATGAGAAGAAGAT 1290
DB 1345 CCTAACTTCAACTTTCATGGGTGAGCTGTGGACTTTCGAGAGGACGCT 1391

RESULT 13
US-09-023-655-946
/ Sequence 946, Application US/09023655
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:

/
/
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023.655
/ FILING DATE: HEREWITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 347:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1208 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: THYNOT03
/ CLONE: 1444245
/ US-09-023-655-347

Query Match 2.8%; Score 94.6; DB 4; Length 1208;
Best Local Similarity 64.3%; Pred. No. 1.5e-18;
Matches 142; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1077 TAGATTTCATTGAGAAAGCAAGCCTCCAAATGGATGTGTTCTAGTGCACCTGTTAGCTG 1136
DB 4 TTGAGTTTCATTGAGGAAGCTCACCAAGTGGGAAGGGGCTTCTCATCCACTGCCAGGCTG 63
QY 1137 GGATCTCCCGCTCCGCCACCATCGCTATCGCTACATCATGAAGAGGATGGACATGTCTT 1196
DB 64 GGGTGTCCCGCTCCGCCACCATCGCTATCGCTTACTTGTATGAAGCACATCCGATGACCA 123
QY 1197 TAGATCAAGCTTACAGATTTGTGAAAGAAAAAGACCTACTATATCTCCAAACTTCAATT 1256
DB 124 TGNCTGATGCTTATAATTTGTCAAGGCCAAGCACCAATTATCTCCCAACCTTAACT 183
QY 1257 TTCTGGGCCAACTCTCGGACTATGAGAAGAAGATTGAAGAC 1297
DB 184 TCATGGGCGAGTTGCTTAGAGTTCGAGGAGACCTAAACAAC 224

RESULT 12
US-09-016-434-1135
/ Sequence 1135, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 946:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2109 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1418933  
US-09-023-655-946

Query Match 2.7%; Score 90.2; DB 4; Length 2109;

Best Local Similarity 57.1%; Pred. No. 5.6e-17;  
Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTCTCGCGTGTGCTGGAATGACAGCTTTTGTGAGAAAATTTTGGCGTGG 1063  
DB 1105 GAGTTTAAATACAAGCAAAATCCCATCTCGGATCACTGGAGCCAAATCCCTGCCAGTTT 1164  
QY 1064 TTGGACAAATCAGTAGATTTCATTGAGAAGCAAAAGCTCCCAATGGATGTTCTAGTG 1123  
DB 1165 TTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGCAAGAACTGTGGTGTCTTGGTA 1224  
QY 1124 CACTGTTTAGCTGGATCTCCGCTCGCCACCATCGCTATCGCTACATCATGAAGAGG 1183  
DB 1225 CATTGCTGGCTGGCATGACCCCTCAGTCAGTGTGCTTACCTTATGCAGAAG 1284  
QY 1184 ATGGACATGTCCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAGAACTACTATATCT 1243  
DB 1285 CTCAATCTGTCGATGAACGATGCTATGACATTGTCAAAATGAAAAATCCACATATCC 1344  
QY 1244 CCAAACTTCAATTTCTGGGCCAACTCTGGACTATGAGAGAAGAT 1290  
DB 1345 CCTAACTTCAACTTTCATGGTGCAGCTGCTGGACTTCGAGAGGACGCT 1391

RESULT 14

US-09-949-016-2615

; Sequence 2615, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2615  
; LENGTH: 2475  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2615

Query Match 2.7%; Score 90.2; DB 4; Length 2475;

Best Local Similarity 57.1%; Pred. No. 6.4e-17;

Matches 164; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 1004 GAGTCTCATTTCTCGCGTGTGCTGGAATGACAGCTTTTGTGAGAAAATTTTGGCGTGG 1063  
DB 1194 GAGTTTAAATACAAGCAAAATCCCATCTCGGATCACTGGAGCCAAATCCCTGCCAGTTT 1253  
QY 1064 TTGGACAAATCAGTAGATTTCATTGAGAAGCAAAAGCTCCCAATGGATGTTCTAGTG 1123  
DB 1254 TTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGCAAGAACTGTGGTGTCTTGGTA 1313  
QY 1124 CACTGTTTAGCTGGATCTCCGCTCGCCACCATCGCTATCGCTACATCATGAAGAGG 1183  
DB 1314 CATTGCTGGCTGGCATTAGCGCTCAGTCACTGTGACTGTGGCTTACCTTATGCAGAAG 1373  
QY 1184 ATGGACATGTCCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAGAACTACTATATCT 1243  
DB 1374 CTCAATCTGTCGATGAACGATGCTTATGACATTGTCAAAATGAAAAATCCACATATCC 1433  
QY 1244 CCAAACTTCAATTTCTGGGCCAACTCTCGGACTATGAGAGAAGAT 1290  
DB 1434 CCTAACTTCAACTTTCATGGTGCAGCTGCTGGACTTCGAGAGGACGCT 1480

RESULT 15

US-09-949-016-14992

; Sequence 14992, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14992

; LENGTH: 13782

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14992

Query Match 2.7%; Score 89.2; DB 4; Length 13782;

Best Local Similarity 69.5%; Pred. No. 5.1e-16;

Matches 121; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 915 TCACCTGCTTGCAGGAGCTGTGATGCAGCAAGATGGGATGTTATGTGTAAATGCCAGCA 974  
DB 9650 TCCGCCCTCCAGATCTGATGACGCAAAATGGAATAGCTACGTCCTCAACGCCAGCA 9709  
QY 975 ATACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGTGCGCTGTGAATG 1034  
DB 9710 ACTCTGTGCCCCAAGCCTGACTTTCATCTGCGAGAGCGCTTTCATGCGGGTCCCATCAACG 9769  
QY 1035 ACAGCTTTTGTGAGAAAATTTTGGCGTGTGCGACAAATCAGTAGATTTTCATTG 1088  
DB 9770 ACAACTACTGTGAAAAAAGTCTGCTGCCCTGTGCGACAAAGTCCATCGAGTTCATCG 9823

Search completed: September 1, 2005, 02:13:59  
Job time : 598 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 31, 2005, 11:02:23 ; Search time 43 Seconds  
(without alignments)  
17.360 Million cell updates

**Title:** US-09-964-277-16  
**Perfect score:** 52  
**Sequence:** 1 VHCLAGISRS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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Database : Issued Patents AA:★
1: /cgn2_6/ptodata/1/aa/5A-COMB pep:★
2: /cgn2_6/ptodata/1/aa/5B-COMB pep:★
3: /cgn2_6/ptodata/1/aa/6A-COMB pep:★
4: /cgn2_6/ptodata/1/aa/6B-COMB pep:★
5: /cgn2_6/ptodata/1/aa/PCtUS-COMB pep:★
6: /cgn2_6/ptodata/1/aa/backfiles1 pep:★
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	52	100.0	87	4	US-09-371-671B-9	Sequence 9, Appli
2	52	100.0	155	4	US-09-955-732A-6	Sequence 6, Appli
3	52	100.0	156	4	US-09-955-732A-3	Sequence 3, Appli
4	52	100.0	156	4	US-09-955-732A-4	Sequence 4, Appli
5	52	100.0	168	4	US-09-544-716-13	Sequence 13, Appli
6	52	100.0	168	4	US-09-557-921-13	Sequence 13, Appli
7	52	100.0	168	4	US-09-564-357-16	Sequence 16, Appli
8	52	100.0	168	4	US-09-619-380-15	Sequence 15, Appli
9	52	100.0	170	4	US-09-544-716-12	Sequence 12, Appli
10	52	100.0	170	4	US-09-544-716-14	Sequence 14, Appli
11	52	100.0	170	4	US-09-557-921-12	Sequence 12, Appli
12	52	100.0	170	4	US-09-557-921-15	Sequence 15, Appli
13	52	100.0	170	4	US-09-564-357-15	Sequence 15, Appli
14	52	100.0	170	4	US-09-564-357-17	Sequence 17, Appli
15	52	100.0	170	4	US-09-619-380-14	Sequence 14, Appli
16	52	100.0	170	4	US-09-619-380-16	Sequence 16, Appli
17	52	100.0	491	4	US-09-949-016-8486	Sequence 8486, Ap
18	52	100.0	661	4	US-09-949-016-9121	Sequence 9121, Ap
19	52	100.0	665	4	US-09-916-494-25	Sequence 2, Appli
20	51	98.1	156	4	US-09-955-732A-5	Sequence 5, Appli
21	51	98.1	207	4	US-09-270-767-44103	Sequence 44103, A
22	51	98.1	421	4	US-09-949-016-10488	Sequence 10488, A
23	48	92.3	226	3	US-09-045-973-8	Sequence 8, Appli
24	46	88.5	11	4	US-09-744-072-32	Sequence 32, Appli
25	46	88.5	23	4	US-09-544-716-5	Sequence 5, Appli
26	46	88.5	23	4	US-09-564-357-6	Sequence 6, Appli
27	46	88.5	24	4	US-09-619-380-4	Sequence 4, Appli

## ALIGNMENTS

```
RESULT 1
US-09-371-671B-9
; Sequence 9, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Chiu, Wan-Ling
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
; FILE OF INVENTION: DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
; CURRENT APPLICATION NUMBER: 00786/370002
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/155,934
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Rat rattus
US-09-371-671B-9

Query Match      100.0%; Score 52; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      34 VHCLAGISRS 43

RESULT 2
US-09-955-732A-6
; Sequence 6, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-6

Query Match      100.0%; Score 52; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      96 VHCLAGISRS 105

RESULT 3
US-09-955-732A-3
; Sequence 3, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
```

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; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-3

Query Match      100.0%; Score 52; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      97 VHCLAGISRS 106

RESULT 4
US-09-955-732A-4
; Sequence 4, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-4

Query Match      100.0%; Score 52; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      97 VHCLAGISRS 106

RESULT 5
US-09-544-716-13
; Sequence 13, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-13

Query Match      100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
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Db      108 VHCLAGISRS 117
|||||
RESULT 6
US-09-557-921-13
; Sequence 13, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-13
Query Match      100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
|||||
Db      108 VHCLAGISRS 117
|||||
RESULT 7
US-09-564-357-16
; Sequence 16, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-16
Query Match      100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
|||||
Db      108 VHCLAGISRS 117
|||||
RESULT 8
US-09-619-380-15
; Sequence 15, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-15
Query Match      100.0%; Score 52; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
|||||
Db      108 VHCLAGISRS 117
|||||
RESULT 9
US-09-544-716-12
; Sequence 12, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-12
Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
|||||
Db      110 VHCLAGISRS 119
|||||
RESULT 10
US-09-544-716-14
; Sequence 14, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-14
Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
|||||
Db      110 VHCLAGISRS 119
|||||
RESULT 11
US-09-557-921-12
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; Sequence 12, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-12

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 12
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-15

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 13
US-09-564-357-15
; Sequence 15, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-15

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 14
US-09-564-357-17
; Sequence 17, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-17

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 15
US-09-619-380-14
; Sequence 14, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-14

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 16
US-09-619-380-16
; Sequence 16, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
```

```
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-16

Query Match      100.0%; Score 52; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 17
US-09-949-016-8486
; Sequence 8486, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8486
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8486

Query Match      100.0%; Score 52; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      401 VHCLAGISRS 410

RESULT 18
US-09-949-016-9121
; Sequence 9121, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 9121
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9121

Query Match      100.0%; Score 52; DB 4; Length 661;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      280 VHCLAGISRS 289

RESULT 19
US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; PHOSPHATASE MOLECULES AND USES THEREFOR
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2

Query Match      100.0%; Score 52; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      242 VHCLAGISRS 251

RESULT 20
US-09-955-732A-5
; Sequence 5, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-5

Query Match      98.1%; Score 51; DB 4; Length 156;
Best Local Similarity 90.0%; Pred. No. 0.028;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      97 VHCLAGISRS 106
```

```
RESULT 21
US-09-270-767-44103
; Sequence 44103, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosoephila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44103
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Drosoephila melanogaster
US-09-270-767-44103

Query Match          98.1%; Score 51; DB 4; Length 207;
Best Local Similarity 90.0%; Pred. No. 0.037;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
      |||||:||||
Db      96 VHCLAGVRS 105

RESULT 22
US-09-949-016-10488
; Sequence 10488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10488
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10488

Query Match          98.1%; Score 51; DB 4; Length 421;
Best Local Similarity 90.0%; Pred. No. 0.078;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
      |||||:||||
Db      325 VHCLAGVRS 334

RESULT 23
US-09-045-973-8
; Sequence 8, Application US/09045973
; Patent No. 6165767
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
; NUMBER OF SEQUENCES: 9
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,973
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0491 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 226 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1495338
US-09-045-973-8

Query Match          92.3%; Score 48; DB 3; Length 226;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
      |||||:||||
Db      96 VHCLAGVRS 105

RESULT 24
US-09-744-072-32
; Sequence 32, Application US/09744072
; Patent No. 6825328
; GENERAL INFORMATION:
; APPLICANT: SCHERER, STEPHEN W.
; APPLICANT: MINASSIAN, BERGE A.
; APPLICANT: ROULEAU, GUY
; APPLICANT: DALGADO-ESCUETA, ANTONIO
; TITLE OF INVENTION: LAFORA'S DISEASE GENE
; FILE REFERENCE: 086671/0113
; CURRENT APPLICATION NUMBER: US/09/744,072
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/093,495
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: 60/130,269
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-744-072-32

Query Match          88.5%; Score 46; DB 4; Length 11;
```



Best Local Similarity 90.0%; Pred. No. 0.015; Indels 1; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VHCLAGISRS 10  
||| |||||  
Db 1 VHCQAGISRS 10

## RESULT 25

US-09-544-716-5  
; Sequence 5, Application US/09544716  
; Patent No. 6492157  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.415  
; CURRENT APPLICATION NUMBER: US/09/544,716  
; CURRENT FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-544-716-5

Query Match 88.5%; Score 46; DB 4; Length 23;  
Best Local Similarity 90.0%; Pred. No. 0.033; Indels 1; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VHCLAGISRS 10  
||| |||||  
Db 5 VHCQAGISRS 14

## RESULT 26

US-09-564-357-6  
; Sequence 6, Application US/09564357  
; Patent No. 6645753  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.413  
; CURRENT APPLICATION NUMBER: US/09/564,357  
; CURRENT FILING DATE: 2000-04-24  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-564-357-6

Query Match 88.5%; Score 46; DB 4; Length 23;  
Best Local Similarity 90.0%; Pred. No. 0.033; Indels 1; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 VHCLAGISRS 10  
||| |||||  
Db 5 VHCQAGISRS 14

## RESULT 27

US-09-619-380-4  
; Sequence 4, Application US/09619380  
; Patent No. 6649391  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.418

; CURRENT APPLICATION NUMBER: US/09/619,380  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-619-380-4

Query Match 88.5%; Score 46; DB 4; Length 24;  
Best Local Similarity 90.0%; Pred. No. 0.035; Indels 1; Gaps 0;  
Matches 9; Conservative 0; Mismatches 1; Gaps 0;

QY 1 VHCLAGISRS 10  
||| |||||  
Db 6 VHCQAGISRS 15

## RESULT 28

US-09-955-732A-17  
; Sequence 17, Application US/09955732A  
; Patent No. 6825021  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.433  
; CURRENT APPLICATION NUMBER: US/09/955,732A  
; CURRENT FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Conserved homology region from eight DSPs having  
; OTHER INFORMATION: MAP-kinase phosphatase activity  
US-09-955-732A-17

Query Match 88.5%; Score 46; DB 4; Length 24;  
Best Local Similarity 90.0%; Pred. No. 0.035; Indels 1; Gaps 0;  
Matches 9; Conservative 0; Mismatches 1; Gaps 0;

QY 1 VHCLAGISRS 10  
||| |||||  
Db 6 VHCQAGISRS 15

## RESULT 29

US-08-530-290-21  
; Sequence 21, Application US/08530290  
; Patent No. 5958721  
; GENERAL INFORMATION:  
; APPLICANT: Marshall, Christopher John  
; APPLICANT: Ashworth, Alan  
; APPLICANT: Hughes, David Anthony  
; TITLE OF INVENTION: Methods for Screening of Substances for  
; TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,290
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB94/00694
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402573.1
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9307250.2
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 084611-000000US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-530-290-21

Query Match      88.5%; Score 46; DB 2; Length 45;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      34 VHCQAGISRS 43

RESULT 30
US-08-530-290-19
; Sequence 19, Application US/08530290
; Patent No. 5958721
; GENERAL INFORMATION:
; APPLICANT: Marshall, Christopher John
; APPLICANT: Ashworth, Alan
; APPLICANT: Hughes, David Anthony
; TITLE OF INVENTION: Methods for Screening of Substances for
; TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,290
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB94/00694
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402573.1
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9307250.2
```

```
;
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 084611-000000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-530-290-19

Query Match      88.5%; Score 46; DB 2; Length 72;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      26 VHCQAGISRS 35

RESULT 31
US-09-371-671B-7
; Sequence 7, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Chiu, Wan-Ling
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
; TITLE OF INVENTION: DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
; FILE REFERENCE: 00786/370002
; CURRENT APPLICATION NUMBER: US/09/371,671B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/155,934
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-371-671B-7

Query Match      88.5%; Score 46; DB 4; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      34 VHCQAGISRS 43

RESULT 32
US-09-371-671B-8
; Sequence 8, Application US/09371671B
; Patent No. 6548743
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Chiu, Wan-Ling
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
; TITLE OF INVENTION: DUAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
; FILE REFERENCE: 00786/370002
; CURRENT APPLICATION NUMBER: US/09/371,671B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/155,934
; PRIOR FILING DATE: 1999-01-14
```

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Query Match	Best Local Similarity	88.5%;	DB 4;	Length 87;	1;	0;	0;
Matches	9;	Conservative	0;	Mismatches	1;	Indels	0;
QY	1 VHCLAGISRS 10						
DB	34 VHCQAGISRS 43						
RESULT 33							
US-07-988-273-4							
Sequence 4, Application US/07988273							
Patent No. 5512434							
GENERAL INFORMATION:							
APPLICANT: AARONSON, Stuart A.							
APPLICANT: BOTTARO, Donald P.							
APPLICANT: ISHIBASHI, Toshio							
APPLICANT: MIKI, Toru							
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN							
TITLE OF INVENTION: PHOSPHATASE							
NUMBER OF SEQUENCES: 7							
CORRESPONDENCE ADDRESS:							
ADDRESSEE: Foley & Lardner							
STREET: 3000 K Street, N.W., Suite 500							
CITY: Washington, D.C.							
COUNTRY: USA							
ZIP: 20007-5109							
COMPUTER READABLE FORM:							
MEDIUM TYPE: Floppy disk							
COMPUTER: IBM PC compatible							
OPERATING SYSTEM: PC-DOS/MS-DOS							
SOFTWARE: Patent In Release #1.0, Version #1.25							
CURRENT APPLICATION DATA:							
APPLICATION NUMBER: US/07/988,273							
FILING DATE: 19921214							
CLASSIFICATION: 435							
ATTORNEY/AGENT INFORMATION:							
NAME: BENT, Stephen A.							
REGISTRATION NUMBER: 29,768							
REFERENCE/DOCKET NUMBER: 40399/182 NIHD							
TELECOMMUNICATION INFORMATION:							
TELEPHONE: (202)672-5300							
TELEFAX: (202)672-5399							
TELEX: 904136							
INFORMATION FOR SEQ ID NO: 4:							
SEQUENCE CHARACTERISTICS:							
LENGTH: 117 amino acids							
TYPE: AMINO ACID							
TOPOLOGY: linear							
US-07-988-273-4							
Query Match	Best Local Similarity	88.5%;	DB 1;	Length 117;	1;	0;	0;
Matches	9;	Conservative	0;	Mismatches	1;	Indels	0;
QY	1 VHCLAGISRS 10						
DB	63 VHCQAGISRS 72						
RESULT 34							
PCT-US93-12019-4							
Sequence 4, Application PC/TUS9312019							
GENERAL INFORMATION:							
APPLICANT: AARONSON, Stuart A.							
APPLICANT: BOTTARO, Donald P.							
APPLICANT: ISHIBASHI, Toshio							
APPLICANT: MIKI, Toru							
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN							
TITLE OF INVENTION: PHOSPHATASE							
NUMBER OF SEQUENCES: 7							
CORRESPONDENCE ADDRESS:							
ADDRESSEE: Foley & Lardner							
STREET: 3000 K Street, N.W., Suite 500							
CITY: Washington, D.C.							
COUNTRY: USA							
ZIP: 20007-5109							
COMPUTER READABLE FORM:							
MEDIUM TYPE: Floppy disk							
COMPUTER: IBM PC compatible							

```
; SEQ ID NO 8
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-8

Query Match      88.5%; Score 46; DB 4; Length 154;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      95 VHCQAGISRS 104

RESULT 37
US-09-955-732A-9
; Sequence 9, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-9

Query Match      88.5%; Score 46; DB 4; Length 154;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      95 VHCQAGISRS 104

RESULT 38
US-09-544-716-15
; Sequence 15, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-15

Query Match      88.5%; Score 46; DB 4; Length 168;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      109 VHCQAGISRS 118

RESULT 39
US-09-557-921-16
; Sequence 16, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-16

Query Match      88.5%; Score 46; DB 4; Length 168;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      109 VHCQAGISRS 118

RESULT 40
US-09-564-357-18
; Sequence 18, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-18

Query Match      88.5%; Score 46; DB 4; Length 168;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
      ||| |||||
Db      109 VHCQAGISRS 118

RESULT 41
US-09-619-380-17
; Sequence 17, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-17
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Query Match      88.5%; Score 46; DB 4; Length 168;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      109 VHCQAGISRS 118

RESULT 42
US-09-544-716-16
; Sequence 16, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-16

Query Match      88.5%; Score 46; DB 4; Length 169;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      109 VHCQAGISRS 118

RESULT 43
US-09-544-716-17
; Sequence 17, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-17

Query Match      88.5%; Score 46; DB 4; Length 169;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      109 VHCQAGISRS 118

RESULT 44
US-09-557-921-17
; Sequence 17, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE

```

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; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-17

Query Match      88.5%; Score 46; DB 4; Length 169;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      109 VHCQAGISRS 118

RESULT 45
US-09-557-921-18
; Sequence 18, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-18

Query Match      88.5%; Score 46; DB 4; Length 169;
Best Local Similarity 90.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      109 VHCQAGISRS 118

Search completed: August 31, 2005, 11:11:30
Job time : 45 secs

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**This Page Blank (uspto)**

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2606	97.7	1998	4	US-09-816-494-3	Sequence 3, Appli
2	2606	97.7	3544	4	US-09-816-494-1	Sequence 1, Appli
3	844	31.6	2377	4	US-09-920-668-3	Sequence 3, Appli
4	842	31.6	2351	4	US-09-949-016-3250	Sequence 3250, Ap
5	741.5	27.8	13782	4	US-09-949-016-14992	Sequence 14992, A
6	308	11.5	2283	4	US-09-949-016-4617	Sequence 4617, Ap
7	308	11.5	2303	4	US-09-922-146-3	Sequence 3, Appli
8	289.5	10.9	1238	4	US-09-702-705-803	Sequence 803, App
9	289.5	10.9	1238	4	US-09-736-457-803	Sequence 803, App
10	289.5	10.9	1238	4	US-09-614-124B-803	Sequence 803, App
11	289.5	10.9	1238	4	US-09-671-325-803	Sequence 803, App
12	289.5	10.9	1238	4	US-09-589-184-803	Sequence 803, App

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Db      341  |||||GCTTCAACTCTGTTACCTGCTTGCA-GGTGGGTTTGTGAGTTCCTCTCGTTGTTTCCT 399
Qy      29  -----
Db      400  GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459
Qy      29  -----
Db      460  GTTGCCAAATTTGGGCCAACCCGAATTTCTCCCAATCTTTATCTTTGGCTGCCAGCGAGAT 519
Qy      30  -----
Db      520  GTTCCTCAACAGAGCTGATGACGAGATGGGATGTTATGTTTAAATGCCGCAAT 579
Qy      46  ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db      580  ACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGCGTGTGCTGTGAATGAC 639
Qy      66  SerPheCysGluLysIleLeuProThrLeuAspLysSerValAspPheIleGluLysAla 85
Db      640  AGCTTTTGTGAGAAAATTTTGGCGGTGGTGGCAAAATCAGTAGATTTTCATTGAGAAAGCA 699
Qy      86  LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db      700  AAAGCCTCCAAATGGATGGTCTAGTGCATCTGTTAGCTGGATCTCCGCTCCGCCACC 759
Qy      106  IleAlaIleAlaTyrlleMetLysArgMetAspMetSerLeuAspGluAlaTyrlzArgPhe 125
Db      760  ATCGCTATCGCTACATCATGATGAAGGATGGACATGTCTTTAGATGAAGCTTACAGATT 819
Qy      126  ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db      820  GTGAAGAAAAGAACCTACTATATCTCCAAATCTTCAATTTTCTGGGCCAATCTCTGGAC 879
Qy      146  TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLysLeu 165
Db      880  TATGAGAAGAAGATTAAAGAACAGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTG 939
Qy      166  LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
Db      940  CTGCACCTGGAGAAGCAAAATGAACCTGTCTCTGCTGTCTCAGAGGGTGGACAGAAAAGC 999
Qy      186  GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db      1000  GAGAGCCCCCTCAGTCCACCTGTGCCGACTCTGTACTCTCAGAGGCGACGAGCAAAAGG 1059
Qy      206  ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db      1060  CCGGTGCATCCCGCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAG 1119
Qy      226  SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db      1120  AGCCCGCTGTGACAGCGCTCAGTGGCTGCACCTGTCCGACAGACAGCGTGGAGACAGC 1179
Qy      246  AsnLysLeuLysArgSerPheSerLeuAspLysSerValSerValSerValSerMet 265
Db      1180  AATAAGCTCAAGCGTTCCTCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATG 1239
Qy      266  AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db      1240  GAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAATATCTACAAACTTCC 1299
Qy      286  ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db      1300  ACTACTCTGGATGGGACCAACAGCTATCCAGTTCCTCCCTGTTCCAGGAATATCGGAG 1359
Qy      306  GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db      1360  CAGACTCCCGAAACCAAGTCTCTATAGAGGAGGAGCCAGCATCCCAAGAGCTGAGACC 1419
Qy      326  AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly

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Db      1420  GCCAGGCTTCAGACAGCCAGAGCAGGATTCATTCGGTTCAGAACCCAGCAGCAGTGCC 1479
Qy      346  ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db      1480  ACCGCCAGAGGTCCCTTTATCTCTCCACTGTCATCGAAGTGGAGCGTGGAGGACAAATTAC 1539
Qy      366  HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db      1540  CACACCAAGCTTCCTTTTCGGCTTTCCACAGCCAGCAGACACCTCAGAACTCTGCTGGC 1599
Qy      386  LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db      1600  CTGGGCTTAAGGCTGGCCTCGCATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 1659
Qy      406  ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db      1660  ACCAGCAGCTGGTATTTTGGCCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 1719
Qy      426  GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db      1720  GGAGGCTAGTCCACTTACTCTGCTCAGCTGCGAGCCAGCTGCCACCTTGGCGGAGACCA 1779
Qy      446  ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgSerTrp 465
Db      1780  GTCTATTCTGTGCGCAGCGCGCAGAACCAAGTCCAGAGAGCTGACTCGCGCGAGCTGG 1839
Qy      466  HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db      1840  CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCGAGAAGCTGCCAAATGGAATTTGGA 1899
Qy      486  GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db      1900  GAGAGCATCATGTCCAGAGAACAGGTCCAGGGAAGAGCTGGGGAAGTGGGCGAGTCACTCT 1959
Qy      506  SerPheSerGlySerMetGluIleGluValSer 517
Db      1960  AGCTTTTCGGGCACATGGAAATCATTTGAGTCTCC 1995

RESULT 2
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIORITY FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)....(2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 2e-256 Length: 3544
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 4 Gaps: 1

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)
Qy      1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArg 20

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Db 869 ATGTTGGCTCTCTCTTCAGACTGTTTCTCACTGTAATCTCTGGTAAACTGGAGAAGA 928  
Qy 21 AlaSerThrLeuPheThrCysLeuGln-----29  
Db 929 GCTTCAACTCTGTTCACTGCTTGCA-GGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCT 987  
Qy 29 -----29  
Db 988 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047  
Qy 29 -----29  
Db 1048 GTTGCCCACTTGGGCCAACCCGAATTTCTCCCAATCTTTATCTTGGCTGCCAGCAGAT 1107  
Qy 30 -----GluLeuMetGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45  
Db 1108 GTCCTCAACAGAGAGCTGATGAGCAGAAATGGATTGGTTATGTGTAAATGCCAGCAAT 1167  
Qy 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65  
Db 1168 ACTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGAC 1227  
Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85  
Db 1228 AGCTTTTGTGAGAAATTTTGGCTGGTGGACAAATCAGTAGATTTCTTCAATGAGAAAGCA 1287  
Qy 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105  
Db 1288 AAGCCCTCAATGGATGTGTTCTAGTACCTGTTAGCTGGATCTCCCGCTCCGCCACC 1347  
Qy 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125  
Db 1348 ATCGCTATCGCTTACATCATGAAGAGATGGACATGCTCTTTAGATGAAGCTTACAGATT 1407  
Qy 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145  
Db 1408 GTGAAGAAATAAGAGACTTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGAC 1467  
Qy 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeu 165  
Db 1468 TATGAGAAGAAGATTAAAGAACAGACTGGAGCATCAGGGCCAAAGACAACTCAAGCTG 1527  
Qy 166 LeuHisLeuGluLysProHsnGluProValProAlaValSerGluGlyGlyLysSer 185  
Db 1528 CTGACCTGGAGAAGCAATAAGAACTGTCCTGCTGCTCTCAGAGGCTGACAGAAAGC 1587  
Qy 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205  
Db 1588 GAGACGCCCTCAGTCCACCTGTCGGACTCTGCTACCTCAGAGGAGCAGACAAAG 1647  
Qy 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225  
Db 1648 CCGGTGCATCCCGCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCTGTTAGAGGAC 1707  
Qy 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245  
Db 1708 AGCCCGCTGTACAGCGCTCAGTGGGCTGCACCTGTCCGACAGACAGGCTGGAAAGCAGC 1767  
Qy 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265  
Db 1768 AATAAGCTCAAGGTTCTCTCTCTGGATATCAATCAGTTTCATATTCAGCCAGCATG 1827  
Qy 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285  
Db 1828 GCAGATCTTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887  
Qy 286 ThrThrLeuAspGlyThrAsnLysLeuLysGlnPheSerProValGlnGluLeuSerGlu 305  
Db 1888 ACTACTCTGATGGGACCAACAGCTATGCCAGTTCCTCCCTGTTTCCAGGAATCTCGAG 1947  
Qy 306 GluThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325

Db 1948 CAGACTCCGAAACCAAGTCTCTGATAAGAGAGAACCCAGCATCCCAAGAACTCGAGACC 2007  
Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345  
Db 2008 GCCAGGCTTTCAGACAGCCAGCAGAGGATTGATTGCTTCGGTCAGAACCCAGCAGTGGC 2067  
Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365  
Db 2068 ACCGCCAGAGGTCCTTTTATCTCTCACTGATCGAAGTGGGAGCGTGGAGCAATTTAC 2127  
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385  
Db 2128 CACACAGCTTCTTTTCGGCTTTTCCACAGCAGCAGCAGCCTTCCAGAGTCTGCTGGC 2187  
Qy 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405  
Db 2188 CTGGGCTTAAGGCTGCGACTCGGATATCTTGGCCCCCAGAGCCTCTACCCCTTCCCTG 2247  
Qy 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425  
Db 2248 ACCAGCAGCTGATATTTTCCACAGAGTCTTACACTTCTTCTCTGCTCAGCCATCTAC 2307  
Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445  
Db 2308 GGAGCAGTGCAGTTACTCTGCTTACAGCTGCAGCAGCTGCCCATTTGGAGACCAA 2367  
Qy 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgSerTrp 465  
Db 2368 GTCTATTTCTGGCAGCGCGCAGAGCAAGTGCAGAGCTGACTCGCGCGGAGCTGG 2427  
Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485  
Db 2428 CATGAAGAGAGCCCTTTGAAAGCAGTTTAAACGCAAGCTGCCAAATGGAATTTGGA 2487  
Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505  
Db 2488 GAGAGCATCATGTTCAGAAACAGGTTCAGGGAAGAGCTGGGGAAGAGTGGGCAGTCA 2547  
Qy 506 SerPheSerGlySerMetGluIleIleGluValSer 517  
Db 2548 AGCTTTTCGGCAGCATGGAAATCATTCAGGCTCTCC 2583

RESULT 3

US-09-920-668-3  
; Sequence 3, Application US/09920668  
; Patent No. 6482644  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION  
; FILE REFERENCE: RTS-0246  
; CURRENT APPLICATION NUMBER: US/09/920,668  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2377  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135) ... (2012)  
US-09-920-668-3

Alignment Scores:  
Pred. No.: 6,828-76 Length: 2377  
Score: 844.00 Matches: 216  
Percent Similarity: 52.99% Conservative: 59  
Best Local Similarity: 41.62% Mismatches: 142  
Query Match: 31.63% Indels: 102  
DB: 4 Gaps: 19

US-09-964-277-21 (1-517) x US-09-920-668-3 (1-2377)

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QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 669 AAGGATCTGATGACCAAAATGAATAAGCTACGTCCTCAACGCCAGCAACTCTGCCCC 728
QY 49 LysProAspPheIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCys 68
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 729 AAGCTGACTTCATCTGCGAGAGCGCTTCATCGGGTCCCATCAACGACAACTACTGT 788
QY 69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 789 GAAAAACTGCTGCCCTGGCTGGACAAAGTCCATCGAGTTTCATCGATAAAGCAAGCTCTCC 848
QY 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 849 AGCTGCCAAGTCACTGTCACCTGTGGCTGGCATCTCCGCTCTGCCACCATGCCATC 908
QY 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 909 GCCTACATCATGAAGACCATGGCATGTCTCCGACGACGCTACAGGTTCTGTGAAGGAC 968
QY 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 969 AGCGCCCGCTCCATCTCGCCCAACTTCAACTTCTCTGGGCCAGCTCTGGAGTACGAGCGC 1028
QY 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1029 ACGCTGAAGCTCTGCGCCCGCTGCGAGGCGACCCGGGC----- 1067
QY 169 GluLysProAsn-----GluProValProAlaValSerGluGlyGlnLysSer 185
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1068 ----ACCCCTCAGGAGCGCGGAGCTCGCCCGAGTCTGCGCGCGGGCGCCCGCTGCCA 1124
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThr-----SerGluAlaAlaGly 203
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1125 CGGCTGCCA-----CCACTACCTCAGAGAGCGGTGCCACAGGGAATGCGGCTGCCAGG 1178
QY 204 GlnArgProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeu 223
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1179 GAGGCGCGCTCAGCGCGCGGCGGAGCCCCCGCGCCCCCACGCCCGCGCGC----- 1232
QY 224 GluAspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGlu 243
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1233 ----ACGAGCGCACTCAGCAGCGGCTGCGCGGCTTCACCTCTCTCGGACCGCTCGAG 1289
QY 244 AspSerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAla 263
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1290 GACACTAACCGCTCAAGGCTCTTCTCCTTGACATCAAGTCTGCC----- 1337
QY 264 SerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLys 283
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1338 -----TACGCC 1343
QY 284 ProSerThrThrLeuAspGlyThrAsn-----LysLeuCys 295
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1344 CTAGCAGCGGCGCCGACGCGCCCGCGGCCCCCGGCGCGGCGGCGCCCGAGCTCTGC 1403
QY 296 GlnPhe---SerPro-----ValGlnGluLeuSerGluGlnThrProGluThrSer 311
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1404 AAGCTGGACAGCGCGCGGGCGCGCGCTGCGGCTGTCTCGCCCGACCGGAC---AGC 1460
QY 312 ProAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSer 331
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1461 CCGGACCGCGCGCTGAGCGCGCCACCGCCCGCGCGCGCGCGCGCGCC----- 1511
QY 332 GlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 351
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1512 -----CCGCGCGGCTCCCGCGCGC----- 1532
QY 352 LeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 371
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1533 ----TCCCCCGCGCAGCGCTCGGC-----CTGAACCTTC 1562
QY 372 Gly-----LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeu 388
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Db 1563 GGCGATCGGCGCGCGAGACTCCCGCGACGGCTCTCGGCCCTGTGGCGCCCGGGCTG 1622
QY 389 LysGly-----TrpHisSerAspIleLeuAlaProGln 399
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1623 CCGGCGCTGGCCAGCGCGCGCGCGCGGCGCTGGGCACCGCGCTTGACTCCCCA--- 1679
QY 400 ThrSerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyr 419
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1680 ---GGCAGCGCGTGCCTCGCGACGGCGCTGTGTGCTTCAGCCCGAG----- 1721
QY 420 SerAlaSerAlaIleTyrGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeu 439
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1722 -----GGCGCACAGGGCGCGGGGTGCTGTGTGGCCCTTCGGCGCGCGGGCGGCC 1775
QY 440 ProThrCysGlyAspGlnValTyrSerValArgArgGlnLysProSerAspArgAla 459
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1776 CCGGACACAGCGCGCGCGACCTCGCGCGCGGAGGAGCGAGGCTTGAGCCCGG 1835
QY 460 AspSerArgArgSerTrpHisGluLysSerProPheGluLysGlnPheLysArgArgSer 479
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1836 GACGCGCGGACCGGCTCGCGCGGAGCGCGCGCGCGCGAGCGCAGTTCAAGCGCGCAGC 1895
QY 480 CysGlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArg---GluGluLeu 498
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1896 TGCCAGATGAGTTTCGAGAGGGC---ATGTTGAGGGCGCGCGCGCGCGAGGAGCTG 1952
QY 499 GlyLysValGlySerGlnSerSerPheSerGlySerMetGluIleLeuValSer 517
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1953 GCGGCCCTGGGCAAGCAGCGGAGCTTCTCGGCGAGCGTGGAGGTTCATCGAGGTGTCC 2009

RESULT 4
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

Alignment Scores:
Pred. No.: 1,07e-75 Length: 2351
Score: 842.00 Matches: 216
Percent Similarity: 52.79% Conservative: 58
Best Local Similarity: 41.62% Mismatches: 143
Query Match: 31.56% Indels: 102
DB: 4

US-09-964-277-21 (1-517) x US-09-949-016-3250 (1-2351)
QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 643 AAGGATCTGATGACGCAAAATGAATAAGCTACGTCCTCAACGCCAGCAACTCTGCCCC 702
QY 49 LysProAspPheIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCys 68
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 703 AAGCTGACTTCATCTGCGAGAGCGGCTTTCATCGGGTCCCCCATCAACGACAACTACTGT 762
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Db 9837 GGGCGGAGGCGAGGACCTGCTAGAGGCTAGAGCTGTGTGTGCCACACACAG 9896
Qy 83 ----- 83
Db 9897 GAGGGTCCCGAGGAAGTAGCGGAAGTGTGGCAGTTGGCGGTGGGGTCCCTACCT 9956
Qy 83 ----- 83
Db 9957 GGGCCAGGAGAGCTGTGCAGTCTTAGCCCTACCTGGCCCCCATGGCCCACTGGCCA 10016
Qy 84 ---LysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArg 102
Db 10017 GATAAGGCAAGCTCTCCAGCTGCGCAAGTCACTGTCCTGCTGGCTGGCATCTCCGC 10076
Qy 103 SerAlaThrIleAlaIleAlaTyrIleMetIysArgMetAspMetSerLeuAspGluAla 122
Db 10077 TCTGCCACCATCGCATCGCTACATCATGAACCATGGCATGTCTCTCCGACGACGCC 10136
Qy 123 Tyr----- 123
Db 10137 TACAGGTACACACTTCCCGAGTCGCGCACTTGTGGCTCACAGCGTCGCTTCCCTTCCGCC 10196
Qy 123 ----- 123
Db 10197 GGCTGCCCACTTGACACAGATGACCCACCGTCCAGACCGGTGGCAAGGAGGAGGC 10256
Qy 123 ----- 123
Db 10257 CTGAGACACCGCTGGCGCACATGAGCTCGTGGGTGCCCGGGTGGCTCAGTGGGCAG 10316
Qy 124 -----ArgPheValIysGluLys 129
Db 10317 CTTGGCCCCGGCGGCGCTGGGACTGAGCTCTCCCGCCGACAGGTTCTGTAAGGACAG 10376
Qy 130 ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLys 149
Db 10377 CGCCGCTCATCTCGCCCACTTCACTTCTGGCCAGCTGCTGGATACGAGCGCAGC 10436
Qy 150 IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlu 169
Db 10437 CTGAAGCTGTGGCGCGCTCGAGGCGACCGCGGC----- 10472
Qy 170 LysProAsn-----GluProValProAlaValSerGluGlyGlnLysSerGlu 186
Db 10473 ACCCGCTCAGGAGCGCGAGGCTCGCGGCTCGCTGCGCGCGGCGCCCGCTGCCACGG 10532
Qy 187 ThrProLeuSerProProCysAlaAspSerAlaThr-----SerGluAlaAlaGlyGln 204
Db 10533 CTGCCA-----CCACTTACCTCAGAGAGCGTGCACAGGAAATCGCGTGCACAGGAG 10586
Qy 205 ArgProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGlu 224
Db 10587 GCGCGCTGAGCGCGGCGGAGCGCCCGCGCCCGCCCGCGCGCGCGCGCG----- 10637
Qy 225 AspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuLeuAsp 244
Db 10638 ACCAGCGCACTCAGAGCGGCTGGCGGCTGCGACCTCTCTCGGACCGCTCGCAGGAC 10697
Qy 245 SerAsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSer 264
Db 10698 ACTAACCGCTCAGCGCTCTCTTCTCCCTGGACATCAAGTCTGCC----- 10742
Qy 265 MetAlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysPro 284
Db 10743 -----TACGCCCT 10751
Qy 285 SerThrThrLeuAspGlyThrAsn-----LysLeuCysGln 296
Db 10752 AGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10811
Qy 297 Phe---SerPro-----ValGlnGluLeuSerGluGlnThrProGluThrSerPro 312
Db 10812 CTGGACAGCCGCTGGGGGCGCGCTGGGCTGTCTCGCCCCATCCCGGAC---AGCCCG 10868
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Qy 313 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 332
Db 10869 GAGCGCGCGCTGATGCGCGCCACAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10916
Qy 333 SerLysArgLeuHisSerValArgThrSerSerGlyThrAlaGlnArgSerLeuLeu 352
Db 10917 -----CCGCGCGCTCTCCCGCGCGCG----- 10937
Qy 353 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 372
Db 10938 TCCCGCGCGCACAGCTCCGCG-----CTGAACCTCGGC 10970
Qy 373 -----LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLys 389
Db 10971 GATCGCGCGCGCAGACTCCGCGCACGCTCTTCGCGCTGTGGCGCGCGCGCGCGCGCG 11030
Qy 390 Gly-----TriHisSerAspIleLeuAlaProGlnThr 400
Db 11031 GGCCCTGGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11084
Qy 401 SerThrProSerLeuThrSerSerTyrPheAlaThrGluSerSerHisPheTyrSer 420
Db 11085 GGCAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11126
Qy 421 AlaSerAlaIleTyrGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
Db 11127 ---GGCGCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11183
Qy 441 ThrCysGlyAspGlnValTyrSerValArgArgGlnLysProSerAspArgAlaAsp 460
Db 11184 GGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11243
Qy 461 SerArgArgSerTrpHisGluSerProPheGluLysGlnPheLysArgArgSerCys 480
Db 11244 GCGCGGACCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11303
Qy 481 GlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArg---GluGluLeuGly 499
Db 11304 CAGATGAGTTCGAGGAGGCG---ATGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 11360
Qy 500 LysValGlySerGlnSerPheSerGlySerMetGluIleLeuGluValSer 517
Db 11361 GCCTGGCGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11414
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## RESULT 6

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US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4617
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4617

Alignment Scores: 6.54e-21 Length: 2283
Pred. No.: 308.00 Matches: 74
Score:
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Percent Similarity: 51.95% Conservative: 46
Best Local Similarity: 32.03% Mismatches: 77
Query Match: 11.54% Indels: 34
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-949-016-4617 (1-2283)

QY 3 ProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgAlaSer 22
Db 699 CCAGTGGGGCTGGGGCATCTTCCTGTCAGATCTGCCCAACCTCTATCTGGGCAT 758
QY 23 ThrLeuPheThrCysLeuGlnGluLeuMetGlnGlnAsnGlylleGlyTyrValLeuAn 42
Db 759 GCCCGGGATTCGCCCAATTTGGAGAGCTGGCCAAATCGGCATCGCTACATCTCAAT 818
QY 43 AlaSerAsnThrCysPro-----LysProAspPheIleProGluSerHis 57
Db 819 GTACCCCCCAACTCCCAACTTCTTCGAGAGATGGTGACTTT-----CAC 866
QY 58 PheLeuArgValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLys 77
Db 867 TACAGCAGATCCCATCTCCGACCATCGGAGCCAGAACCTGTCGGGTCTTTCGGGAG 926
QY 78 SerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeu 97
Db 927 GCCATTGAGTTGATGAGGCTTGTCCAGAACTGGCGGGTGTCTGTCACCTGCTT 986
QY 98 AlaGlylleSerArgSerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMet 117
Db 987 GCGGGGGTGGCGGTCTGTACCGTCTGTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1046
QY 1047 TCTCTCAAGATGCCTATGACCTGTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1106
QY 138 AsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAlaGlnThrGlyAlaSer 157
Db 1107 AACTTCATGGGCGAGTTGTCGACTTTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1145
QY 158 GlyProLysSerLysLeuLysLeuHisLeuGluLysProAsnGluProValProAla 177
Db 1146 -----CGGCTGGAGGAGCGCCACTCGCAGGAGCAG-----1175
QY 178 ValSerGluGlyGlnLysSerGluThrProLeuSerPro-----Pro 192
Db 1176 ----GGCAGTGGGGGCGAGCATCTGGGCTCCAAACCGCCCTCTCTTTCACACCCCC 1232
QY 193 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProVal-----HisProAla 210
Db 1233 ACCAGTGATGGGCGCTTCGAGCTGGCGCCCACTAGGCGCGCGTGGCGGCGCGCC 1292

RESULT 7
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: R1S-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (114)...(1268)
US-09-922-146-3
Alignment Scores:
Pred. No.: 6,646-21 Length: 2303
Score: 208.00 Matches: 74
Percent Similarity: 51.95% Conservative: 46
Best Local Similarity: 32.03% Mismatches: 77
Query Match: 11.54% Indels: 34
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-922-146-3 (1-2303)

QY 3 ProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgAlaSer 22
Db 699 CCAGTGGGGCTGGGGCATCTTCCTGTCAGATCTGCCCAACCTCTATCTGGGCAT 758
QY 23 ThrLeuPheThrCysLeuGlnGluLeuMetGlnGlnAsnGlylleGlyTyrValLeuAn 42
Db 759 GCCCGGGATTCGCCCAATTTGGAGAGCTGGCCAAATCGGCATCGCTACATCTCAAT 818
QY 43 AlaSerAsnThrCysPro-----LysProAspPheIleProGluSerHis 57
Db 819 GTACCCCCCAACTCCCAACTTCTTCGAGAGATGGTGACTTT-----CAC 866
QY 58 PheLeuArgValProValAsnAspSerPheCysGluLysIleLeuProTrpLeuAspLys 77
Db 867 TACAGCAGATCCCATCTCCGACCATCGGAGCCAGAACCTGTCGGGTCTTTCGGGAG 926
QY 78 SerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysValLeuValHisCysLeu 97
Db 927 GCCATTGAGTTGATGAGGCTTGTCCAGAACTGGCGGGTGTCTGTCACCTGCTT 986
QY 98 AlaGlylleSerArgSerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMet 117
Db 987 GCGGGGGTGGCGGTCTGTACCGTCTGTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1046
QY 1047 TCTCTCAAGATGCCTATGACCTGTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1106
QY 138 AsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAlaGlnThrGlyAlaSer 157
Db 1107 AACTTCATGGGCGAGTTGTCGACTTTCAGAGAGAGAGTCTAACATCTCCCCAACTTC 1145
QY 158 GlyProLysSerLysLeuLysLeuHisLeuGluLysProAsnGluProValProAla 177
Db 1146 -----CGGCTGGAGGAGCGCCACTCGCAGGAGCAG-----1175
QY 178 ValSerGluGlyGlnLysSerGluThrProLeuSerPro-----Pro 192
Db 1176 ----GGCAGTGGGGGCGAGCATCTGGGCTCCAAACCGCCCTCTCTTTCACACCCCC 1232
QY 193 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProVal-----HisProAla 210
Db 1233 ACCAGTGATGGGCGCTTCGAGCTGGCGCCCACTAGGCGCGCGTGGCGGCGCGCC 1292

RESULT 8
US-09-702-705-803
; Sequence 803, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
```

```
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-803

Alignment Scores:
Pred. No.: 1,73e-19 Length: 1238
Score: 289.50 Matches: 72
Percent Similarity: 54.15% Conservative: 39
Best Local Similarity: 35.12% Mismatches: 69
Query Match: 10.85% Indels: 25
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-702-705-803 (1-1238)
QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
Db 693 AGAGACATCGTGGAGCCCGCTGGCATCAGCGCTCTGTTGAATGTCCTCGGACTGCCCA 752
QY 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
Db 753 AAC---CACTTTGAAGGACACTATCAGTACAAAGTCATCCAGTGGAGAGATAACCAACAG 809
QY 69 GluLysIleLeuProTrrPheLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
Db 810 GCGGACATCAGCTCTGTTTCATGGAAGCCATAGATACATGATCGATCGGTGAAGACTGC 869
QY 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
Db 870 CGTGGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 929
QY 109 AlaTyrIleMetLysArgMetSerLysSerValAspGluAlaTyrArgPheValLysGlu 128
Db 930 GCCTACCTGATGATGAAGAAACGGGTGAGCTGGAGAGGCGCTTCGAGTTTCGTTAAGCAG 989
QY 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGluLys 148
Db 990 CGCCGCGAGCATCATCTGCCCACTTCAGTTTCATGGGCGAGCTGCTGAGTTTCGAGTCC 1049
QY 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLysLeuHisLeu 168
Db 1050 CAGGTGCTGGCCACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1088
QY 169 GluLysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrPro 188
Db 1089 -----CCCTCGGAGCCCTG-----GGGAGCGGGGCAAGACCCCC 1124
QY 189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208
Db 1125 GCCACCCCC-----ACCTCGCAGTTCGTTTCAGCTTTCGGGTC--- 1163
QY 209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228
Db 1164 TCGGTGGGCGTCACTCGGCCCCCGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1217
QY 229 ValGlnAlaLeuSer 233
Db 1218 ACCACCTCTCCACG 1232

RESULT 9
US-09-736-457-803
; Sequence 803, Application US/09736457
; Patent No. 6509448
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QY 189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208  
 Db 1125 GCCACCCCC-----ACCTCGCAGTTTCGTTCCGATCTTCCGATC--- 1163  
 QY 209 ProAlaSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228  
 Db 1164 TCCGTGGCGGTGACTCGGCCCCGACGAGCTGCTACCTG-----CACAGCCCATC 1217  
 QY 229 ValGlnAlaLeuSer 233  
 Db 1218 ACCACCTCTCCAGC 1232  
 RESULT 11  
 US-09-671-325-803  
 ; Sequence 803, Application US/09671325  
 ; Patent No. 6667154  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Lodes, Michael A.  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Vedvick, Tom  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Fan, Liqun  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.478C12  
 ; CURRENT APPLICATION NUMBER: US/09/671,325  
 ; CURRENT FILING DATE: 2000-09-26  
 ; NUMBER OF SEQ ID NOS: 1825  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 803  
 ; LENGTH: 1238  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-671-325-803  
 Alignment Scores:  
 Pred. No.: 1,738-19 Length: 1238  
 Score: 289.50 Matches: 72  
 Percent Similarity: 54.15% Conservative: 39  
 Best Local Similarity: 35.12% Mismatches: 69  
 Query Match: 10.85% Indels: 25  
 DB: 4 Gaps: 6  
 US-09-964-277-21 (1-517) x US-09-671-325-803 (1-1238)  
 QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48  
 Db 693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTGAATGCTCTCGGACTGCCCA 752  
 QY 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68  
 Db 753 AAC---CACTTTGAAGGACACTATCAGTACAAAGTGCATCCAGTGGAGATACCAACAAG 809  
 QY 69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88  
 Db 810 GCCGACATCAGTCCTCGGTTCATGGAAGCCATAGAGTACATCATGCTCGGAGGACTGC 869  
 QY 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108  
 Db 870 CGTGGCGGTGCTGGTGCACTGCCAGGGGGCACTCTCGCGTCCGCCACCATCTGCCTG 929  
 QY 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128  
 Db 930 GCCTACCTGATGATGAAGAAACGGGTGAGCTGGAGAGGCGCTTCGAGTTCGTTAAGCAG 989  
 QY 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGluLys 148  
 Db 990 CGCCGACGACATCATCTCGCCCAACTTCAGCTTCATGGGCGAGCTGTGTCAGTTTCGAGTCC 1049  
 Db 990 CGCCGACGACATCATCTCGCCCAACTTCAGCTTCATGGGCGAGCTGTGTCAGTTTCGAGTCC 1049

QY 229 ValGlnAlaLeuSer 233  
 Db 1218 ACCACCTCTCCAGC 1232  
 RESULT 10  
 US-09-614-124B-803  
 ; Sequence 803, Application US/09614124B  
 ; Patent No. 6630574  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Lodes, Michael A.  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Vedvick, Tom  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Mannion, Jane  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.478C9  
 ; CURRENT APPLICATION NUMBER: US/09/614,124B  
 ; CURRENT FILING DATE: 2001-07-11  
 ; NUMBER OF SEQ ID NOS: 1668  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 803  
 ; LENGTH: 1238  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-614-124B-803  
 Alignment Scores:  
 Pred. No.: 1,738-19 Length: 1238  
 Score: 289.50 Matches: 72  
 Percent Similarity: 54.15% Conservative: 39  
 Best Local Similarity: 35.12% Mismatches: 69  
 Query Match: 10.85% Indels: 25  
 DB: 4 Gaps: 6  
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 QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48  
 Db 693 AGAGACATGCTGGACGCCCTGGGCATCACGGCTCTGTGAATGCTCTCGGACTGCCCA 752  
 QY 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68  
 Db 753 AAC---CACTTTGAAGGACACTATCAGTACAAAGTGCATCCAGTGGAGATACCAACAAG 809  
 QY 69 GluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88  
 Db 810 GCCGACATCAGTCCTCGGTTCATGGAAGCCATAGAGTACATCATGCTCGGAGGACTGC 869  
 QY 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108  
 Db 870 CGTGGCGGTGCTGGTGCACTGCCAGGGGGCACTCTCGCGTCCGCCACCATCTGCCTG 929  
 QY 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128  
 Db 930 GCCTACCTGATGATGAAGAAACGGGTGAGCTGGAGAGGCGCTTCGAGTTCGTTAAGCAG 989  
 QY 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGluLys 148  
 Db 990 CGCCGACGACATCATCTCGCCCAACTTCAGCTTCATGGGCGAGCTGTGTCAGTTTCGAGTCC 1049  
 QY 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeuLeuHisLeu 168  
 Db 1050 CAGTGTGGCCAGCTCTGTGCTGGAGGCTGCTAGC----- 1088  
 QY 169 GluLysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrPro 188  
 Db 1089 -----CCCTCGGACCCCTG-----GGGAGCGGGGCAAGACCCCC 1124





Db 810 GCCGACATCAGCTCTCGTTCATGGAAGCCATAGAGTACATCGATCGCGTGAAGGACTGC 869  
Qy 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108  
Db 870 CCGTGGCGGCTGCTGGTGCACATGCGAGGGGCGATCTCGCGTGGCCACCATCTGCCTG 929  
Qy 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128  
Db 930 GCCTACCTGATGATGAAGAACGGGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAG 989  
Qy 129 LysArgProThrIleSerProAsnPheAsnGlyGlnLeuLeuAspTyrGluLys 148  
Db 990 CGCCGAGCATCATCTCGCCCACTTCAGTTTCATGGGCGAGCTGCTGCAGTTCGAGTCC 1049  
Qy 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeu 168  
Db 1050 CAGGTGCTGCCACGCTCTGCTGCGGAGGCTGTAGC----- 1088  
Qy 169 GluLysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrPro 188  
Db 1089 -----CCCTCGGACCCCTG-----GGGAGCGGGGCAAGACCC 1124  
Qy 189 LeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHis 208  
Db 1125 GCCACCCCTC-----ACCTGCGAGTTCGCTTTCAGCTTTCGCGTCTC--- 1163  
Qy 209 ProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeu 228  
Db 1164 TCGTGGGGGTGCATCGGCCGCCAGCAGCCTGCTACCTG-----CACAGCCCATC 1217  
Qy 229 ValGlnAlaLeuSer 233  
Db 1218 ACCACCTCTCCAGC 1232

RESULT 14  
US-09-702-705-801  
; Sequence 801, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702,705  
; CURRENT FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 801  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-801

Alignment Scores:  
Pred. No.: 5.05e-19 Length: 1619  
Score: 287.00  
Percent Similarity: 55.02%  
Best Local Similarity: 34.93%  
Query Match: 10.76%  
DB: 4  
Matches: 73  
Conservative: 42  
Mismatch: 69  
Indels: 25  
Gaps: 6

US-09-964-277-21 (1-517) x US-09-702-705-801 (1-1619)

Qy 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48

Db 365 AGAGACATGCTGGAGCCCTCGGCTACAGGCTCTGTTGAATGTCTCTCGAGCTGCCCA 424  
Qy 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68  
Db 425 AAC---CACTTTGAAGNACATATCAGTACAGTGCATCCAGTGGAGATAACCAAG 481  
Qy 69 GluLysIleLeuProTyrPheLysSerValAspPheIleGluLysAlaLysAlaSer 88  
Db 482 GCCGACATCAGCTCTCGTTCATGAGCCATAGAGTACATCGATCGCGTGAAGGACTGC 541  
Qy 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108  
Db 542 CCGTGGCGGCTGCTGGTGCATGCGAGGGGCGATCTCGCGTGGCCACCATCTGCCTG 601  
Qy 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128  
Db 602 GCCTACCTGATGATGAAGAACGGGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAG 661  
Qy 129 LysArgProThrIleSerProAsnPheAsnGlyGlnLeuLeuAspTyrGluLys 148  
Db 662 CGCGCAGCATATCTCGCCCACTTCAGTTTCATGGGCGAGCTGCTGCAGTTCGAGTCC 721  
Qy 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeu 168  
Db 722 CAGGTGCTGGCCACGCTCTGCTGCGGAGGCTGTAGC----- 760  
Qy 169 GluLysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrPro 188  
Db 761 -----CCCTCGGACCCCTG-----CGGAGCGGGGCAAGACCC 796  
Qy 189 LeuSer-ProProCysAlaAspSerAlaThr-----SerGluAlaAlaGlyGlnArgPr 206  
Db 797 GCCACCCCATCCTCGCAGTTCGCTTTCAGCTTTCGCGTCTCGTGGGCGTGCACCTCGGCC 856  
Qy 206 oValHisProAlaSerValProSerValGlnProSerValGlnProSerLeuLeuGluAspSe 226  
Db 857 C-----CCAGCAGCCTGCTTACCTGCACAGCCCATCACCACCTCTC----- 899  
Qy 226 rProLeuValGlnAlaLeuSerGly 234  
Db 900 -CCAGCTGTAGAGCCGCTCGGG 923

RESULT 15  
US-09-736-457-801  
; Sequence 801, Application US/09736457  
; Patent No. 6509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; APPLICANT: Wang, Aijun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C15  
; CURRENT APPLICATION NUMBER: US/09/736,457  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 1864  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 801  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-736-457-801

Alignment Scores:  
Pred. No.: 5.05e-19 Length: 1619

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Score: 287.00 Matches: 73
Percent Similarity: 55.02% Conservative: 42
Best Local Similarity: 34.93% Mismatches: 69
Query Match: 10.76% Indels: 25
DB: 4 Gaps: 6

US-09-964-277-21 (1-517) x US-09-736-457-801 (1-1619)

QY 29 GlnGluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsnThrCysPro 48
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
365 AGAGACATGCTGGACGCCCTGGGCATCAGGGCTGTGTTGAATGTCTCTCGGACTGCCCA 424
QY 49 LysProAspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCys 68
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
425 AAC---CACTTTGAAGGACACTATCAGTACAAAGTGCATCCCAAGTGAAGATAACCAACAG 481
QY 69 GluLysIleLeuProThrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSer 88
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
482 GCCGACATCAGCTCTGTGTTTCATGGAAGCCATAGAGTACATCGATGCCGTGAAGACTGC 541
QY 89 AsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIle 108
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
542 CGTGGCGCGTCTGTGTCACCTGCCAGCGGGCATCTCGGGTGGGCCACCATCTGCCTG 601
QY 109 AlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlu 128
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
602 GCCTACCTGATGATGAAGAAACGGGTGAGGCTGGAGAGGCCCTCGAGTTCGTTAAGCAG 661
QY 129 LysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLys 148
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
662 CCGCCGAGCATTATCTGCCCAACTTCAGCTTCATGGGGCAGCTGCTGCAGTTCGAGTCC 721
QY 149 LysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeu 168
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
722 CAGGTCTGCCACGTCCTGTGCTGGAGGCTGTAGC----- 760
QY 169 GluLysProAsnGluProValProAlaValSerGluGlyGlnLysSerGluThrPro 188
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
761 -----CCCTCGGAGCCCTG-----CGGGAGCGGGGCAAGACCCCC 796
QY 189 LeuSer-ProProCysAlaAspSerAlaThr-----SerGluAlaAlaGlyGlnArgPr 206
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
797 GCCACCCCACTCGCAGTTCGTCTTCAGCTTCCGGTCTCCGTGGGCGTGCACTCGGCC 856
QY 206 oValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAspSe 226
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
857 C-----CCAGCAGCCTGCCCTACCTGCACACCCCATCACCACTCTC----- 899
QY 226 rProLeuValGlnAlaLeuSerGly 234
Db ::::::::::: ||||| ::::::::::: ||||| ::::::::::: |||||
900 -CCAGCTGTAGAGCGCCCTGGGG 923
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Job time : 396 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 31, 2005, 11:02:23 ; Search time 159 Seconds

(without alignments)  
24.712 Million cell updates/sec

Title: US-09-964-277-16

Perfect score: 52

Sequence: 1 VHCLAGISRS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 22: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	52	100.0	23	18	US-10-029-345A-144
4	52	100.0	41	9	US-09-964-277-13
5	52	100.0	140	17	US-10-803-738-12
6	52	100.0	140	18	US-10-029-345A-134
7	52	100.0	141	17	US-10-803-738-7
8	52	100.0	141	17	US-10-803-738-8
9	52	100.0	155	9	US-09-964-277-6
10	52	100.0	155	9	US-09-964-277-7
11	52	100.0	155	9	US-09-955-732-6

12	52	100.0	156	9	US-09-964-277-3	Sequence 3, Appli
13	52	100.0	156	9	US-09-964-277-4	Sequence 4, Appli
14	52	100.0	156	9	US-09-955-732-3	Sequence 3, Appli
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16	52	100.0	167	14	US-10-346-356-13	Sequence 13, Appli
17	52	100.0	168	9	US-09-775-925-24	Sequence 24, Appli
18	52	100.0	168	9	US-09-847-519A-9	Sequence 9, Appli
19	52	100.0	168	14	US-10-314-058-13	Sequence 13, Appli
20	52	100.0	168	14	US-10-405-078-15	Sequence 15, Appli
21	52	100.0	168	15	US-10-655-073-15	Sequence 15, Appli
22	52	100.0	168	17	US-10-962-126-24	Sequence 24, Appli
23	52	100.0	168	17	US-10-644-554-16	Sequence 16, Appli
24	52	100.0	168	18	US-10-658-661-12	Sequence 12, Appli
25	52	100.0	169	14	US-10-346-356-12	Sequence 12, Appli
26	52	100.0	169	14	US-10-346-356-15	Sequence 15, Appli
27	52	100.0	170	9	US-09-775-925-23	Sequence 23, Appli
28	52	100.0	170	9	US-09-775-925-26	Sequence 26, Appli
29	52	100.0	170	9	US-09-847-519A-8	Sequence 8, Appli
30	52	100.0	170	9	US-09-847-519A-11	Sequence 11, Appli
31	52	100.0	170	14	US-10-314-058-12	Sequence 12, Appli
32	52	100.0	170	14	US-10-314-058-14	Sequence 14, Appli
33	52	100.0	170	14	US-10-405-080-14	Sequence 14, Appli
34	52	100.0	170	14	US-10-405-080-16	Sequence 16, Appli
35	52	100.0	170	15	US-10-655-073-16	Sequence 16, Appli
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39	52	100.0	170	17	US-10-644-554-17	Sequence 17, Appli
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41	52	100.0	170	18	US-10-658-661-13	Sequence 13, Appli
42	52	100.0	170	18	US-10-658-661-13	Sequence 13, Appli
43	52	100.0	189	9	US-09-925-299-842	Sequence 842, App
44	52	100.0	189	10	US-09-925-299-842	Sequence 842, App
45	52	100.0	302	18	US-10-029-345A-191	Sequence 191, App
46	52	100.0	322	14	US-10-060-065-33	Sequence 33, Appli
47	52	100.0	322	14	US-10-059-585-54	Sequence 54, Appli
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49	52	100.0	381	18	US-10-029-345A-111	Sequence 111, App
50	52	100.0	419	16	US-10-472-380-2	Sequence 2, Appli
51	52	100.0	501	15	US-10-072-012-702	Sequence 702, App
52	52	100.0	517	9	US-09-964-277-21	Sequence 21, Appli
53	52	100.0	625	15	US-10-072-012-699	Sequence 699, App
54	52	100.0	625	18	US-10-029-345A-39	Sequence 39, Appli
55	52	100.0	625	18	US-10-029-345A-110	Sequence 110, App
56	52	100.0	662	15	US-10-072-012-258	Sequence 258, App
57	52	100.0	663	15	US-10-072-012-700	Sequence 700, App
58	52	100.0	663	18	US-10-029-345A-40	Sequence 40, Appli
59	52	100.0	664	18	US-10-029-345A-190	Sequence 190, App
60	52	100.0	665	9	US-09-816-494-2	Sequence 2, Appli
61	52	100.0	665	9	US-09-964-277-2	Sequence 2, Appli
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65	52	100.0	665	15	US-10-072-012-681	Sequence 681, App
66	52	100.0	665	15	US-10-168-506-14	Sequence 14, Appli
67	52	100.0	665	15	US-10-343-357-7	Sequence 7, Appli
68	52	100.0	665	15	US-10-257-026-2	Sequence 2, Appli
69	52	100.0	665	16	US-10-648-593-240	Sequence 240, App
70	52	100.0	665	16	US-10-648-593-247	Sequence 247, App
71	52	100.0	665	16	US-10-377-072-26	Sequence 26, Appli
72	52	100.0	665	16	US-10-370-715B-262	Sequence 262, App
73	52	100.0	665	17	US-10-838-181-14	Sequence 14, Appli
74	52	100.0	665	18	US-10-029-345A-42	Sequence 42, Appli
75	52	100.0	665	18	US-10-029-345A-109	Sequence 109, App
76	52	100.0	665	18	US-10-029-345A-148	Sequence 148, App
77	52	100.0	672	15	US-10-296-115-1359	Sequence 1259, App
78	52	100.0	680	15	US-10-072-012-256	Sequence 256, App
79	52	100.0	690	15	US-10-072-012-679	Sequence 679, App
80	52	100.0	690	15	US-10-072-012-703	Sequence 703, App
81	52	100.0	690	15	US-10-425-114-54204	Sequence 54204, A
82	51	98.1	10	18	US-10-658-661-3	Sequence 3, Appli
83	51	98.1	92	16	US-10-425-115-335209	Sequence 335209,
84	51	98.1	138	17	US-10-803-738-5	Sequence 5, Appli

85 51 98.1 140 18 US-10-029-345A-135 Sequence 135, Appl  
86 51 98.1 141 17 US-10-803-738-9 Sequence 9, Appl  
87 51 98.1 145 18 US-10-658-661-19 Sequence 19, Appl  
88 51 98.1 156 9 US-09-964-277-5 Sequence 5, Appl  
89 51 98.1 156 9 US-09-955-732-5 Sequence 5, Appl  
90 51 98.1 157 9 US-09-775-925-25 Sequence 25, Appl  
91 51 98.1 157 9 US-09-847-519A-10 Sequence 10, Appl  
92 51 98.1 157 17 US-10-962-126-25 Sequence 25, Appl  
93 51 98.1 162 15 US-10-104-047-3471 Sequence 3471, Ap  
94 51 98.1 179 15 US-10-296-115-1179 Sequence 1179, Ap  
95 51 98.1 184 14 US-10-151-320-15 Sequence 15, Appl  
96 51 98.1 184 14 US-10-287-806-2 Sequence 2, Appl  
97 51 98.1 184 15 US-10-264-237-2811 Sequence 2811, Ap  
98 51 98.1 184 15 US-10-072-012-428 Sequence 428, App  
99 51 98.1 184 15 US-10-072-012-429 Sequence 429, App  
100 51 98.1 184 15 US-10-072-012-430 Sequence 430, App

## ALIGNMENTS

## RESULT 1

US-09-964-277-16  
; Sequence 16, Application US/09964277  
; Patent No. US20020137170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.434  
; CURRENT APPLICATION NUMBER: US/09/964,277  
; CURRENT FILING DATE: 2001-09-25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-277-16

Query Match 100.0%; Score 52; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0071;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 1 VHCLAGISRS 10

## RESULT 2

US-10-029-345A-103  
; Sequence 103, Application US/10029345A  
; Publication No. US20050130286A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES  
; FILE REFERENCE: D0072.NP  
; CURRENT APPLICATION NUMBER: US/10/029,345A  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/256,868  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 60/280,186  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/287,735  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 60/295,848  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/300,465  
; PRIOR FILING DATE: 2001-06-25  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 103  
; LENGTH: 23

; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-029-345A-103

Query Match 100.0%; Score 52; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 6 VHCLAGISRS 15

## RESULT 3

US-10-029-345A-144  
; Sequence 144, Application US/10029345A  
; Publication No. US20050130286A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES  
; FILE REFERENCE: D0072.NP  
; CURRENT APPLICATION NUMBER: US/10/029,345A  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/256,868  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 60/280,186  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/287,735  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 60/295,848  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/300,465  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 144  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-345A-144

Query Match 100.0%; Score 52; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 6 VHCLAGISRS 15

## RESULT 4

US-09-964-277-13  
; Sequence 13, Application US/09964277  
; Patent No. US20020137170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.434  
; CURRENT APPLICATION NUMBER: US/09/964,277  
; CURRENT FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-277-13

Query Match 100.0%; Score 52; DB 9; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 |||||  
 Db 11 VHCLAGISRS 20

RESULT 5

US-10-803-738-12  
 ; Sequence 12, Application US/10803738  
 ; Publication No. US20050014222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Belmont, John  
 ; APPLICANT: Fletcher, Frederick  
 ; APPLICANT: Chen, Alice  
 ; APPLICANT: Jurecic, Roland  
 ; APPLICANT: Colicos, Suzanne  
 ; APPLICANT: Tan, Tse-Hua  
 ; APPLICANT: Zhou, Guisheng  
 ; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
 ; FILE REFERENCE: 99-383-B  
 ; CURRENT APPLICATION NUMBER: US/10/803,738  
 ; CURRENT FILING DATE: 2004-03-18  
 ; PRIOR APPLICATION NUMBER: US/09/665,819A  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US 60/155,068  
 ; PRIOR FILING DATE: 1999-09-21  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 140  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: MH3/6  
 US-10-803-738-12

Query Match 100.0%; Score 52; DB 17; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 0.098;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 |||||  
 Db 84 VHCLAGISRS 93

RESULT 6

US-10-029-345A-134  
 ; Sequence 134, Application US/10029345A  
 ; Publication No. US20050130286A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES  
 ; FILE REFERENCE: D0072.NP  
 ; CURRENT APPLICATION NUMBER: US/10/029,345A  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/256,868  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/280,186  
 ; PRIOR FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: US 60/287,735  
 ; PRIOR FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/295,848  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/300,465  
 ; PRIOR FILING DATE: 2001-06-25  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 134  
 ; LENGTH: 140  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-029-345A-134

Query Match 100.0%; Score 52; DB 18; Length 140;

Best Local Similarity 100.0%; Pred. No. 0.098;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 |||||  
 Db 85 VHCLAGISRS 94

RESULT 7

US-10-803-738-7  
 ; Sequence 7, Application US/10803738  
 ; Publication No. US20050014222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Belmont, John  
 ; APPLICANT: Fletcher, Frederick  
 ; APPLICANT: Chen, Alice  
 ; APPLICANT: Jurecic, Roland  
 ; APPLICANT: Colicos, Suzanne  
 ; APPLICANT: Tan, Tse-Hua  
 ; APPLICANT: Zhou, Guisheng  
 ; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
 ; FILE REFERENCE: 99-383-B  
 ; CURRENT APPLICATION NUMBER: US/10/803,738  
 ; CURRENT FILING DATE: 2004-03-18  
 ; PRIOR APPLICATION NUMBER: US/09/665,819A  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US 60/155,068  
 ; PRIOR FILING DATE: 1999-09-21  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 141  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: rMKP-3  
 US-10-803-738-7

Query Match 100.0%; Score 52; DB 17; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 0.098;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 |||||  
 Db 85 VHCLAGISRS 94

RESULT 8

US-10-803-738-8  
 ; Sequence 8, Application US/10803738  
 ; Publication No. US20050014222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Belmont, John  
 ; APPLICANT: Fletcher, Frederick  
 ; APPLICANT: Chen, Alice  
 ; APPLICANT: Jurecic, Roland  
 ; APPLICANT: Colicos, Suzanne  
 ; APPLICANT: Tan, Tse-Hua  
 ; APPLICANT: Zhou, Guisheng  
 ; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
 ; FILE REFERENCE: 99-383-B  
 ; CURRENT APPLICATION NUMBER: US/10/803,738  
 ; CURRENT FILING DATE: 2004-03-18  
 ; PRIOR APPLICATION NUMBER: US/09/665,819A  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US 60/155,068  
 ; PRIOR FILING DATE: 1999-09-21  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 141  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: rMKP-3  
 US-10-803-738-8

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: rMKP-X  
US-10-803-738-8

Query Match 100.0%; Score 52; DB 17; Length 141;  
Best Local Similarity 100.0%; Pred. No. 0.098; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
DB 85 VHCLAGISRS 94

## RESULT 9

US-09-964-277-6

; Sequence 6, Application US/09964277  
; Patent No. US20020137170A1

; GENERAL INFORMATION:

; APPLICANT: Luche, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.434

; CURRENT APPLICATION NUMBER: US/09/964,277

; CURRENT FILING DATE: 2001-09-25

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 155

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-964-277-6

Query Match 100.0%; Score 52; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
DB 96 VHCLAGISRS 105

## RESULT 10

US-09-964-277-7

; Sequence 7, Application US/09964277

; Patent No. US20020137170A1

; GENERAL INFORMATION:

; APPLICANT: Luche, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.434

; CURRENT APPLICATION NUMBER: US/09/964,277

; CURRENT FILING DATE: 2001-09-25

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 155

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-964-277-7

Query Match 100.0%; Score 52; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
DB 96 VHCLAGISRS 105

## RESULT 11

US-09-955-732-6

; Sequence 6, Application US/09955732

; Publication No. US20020182203A1

; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.433

; CURRENT APPLICATION NUMBER: US/09/955,732

; CURRENT FILING DATE: 2001-09-18

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 155

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-955-732-6

Query Match 100.0%; Score 52; DB 9; Length 155;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
DB 96 VHCLAGISRS 105

## RESULT 12

US-09-964-277-3

; Sequence 3, Application US/09964277

; Patent No. US20020137170A1

; GENERAL INFORMATION:

; APPLICANT: Luche, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.434

; CURRENT APPLICATION NUMBER: US/09/964,277

; CURRENT FILING DATE: 2001-09-25

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 156

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-964-277-3

Query Match 100.0%; Score 52; DB 9; Length 156;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
DB 97 VHCLAGISRS 106

## RESULT 13

US-09-964-277-4

; Sequence 4, Application US/09964277

; Patent No. US20020137170A1

; GENERAL INFORMATION:

; APPLICANT: Luche, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.434

; CURRENT APPLICATION NUMBER: US/09/964,277

; CURRENT FILING DATE: 2001-09-25

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 156

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-964-277-4

Query Match 100.0%; Score 52; DB 9; Length 156;  
Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 97 VHCLAGISRS 106

## RESULT 14

US-09-955-732-3

; Sequence 3, Application US/09955732  
; Publication No. US20020182203A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.433  
; CURRENT APPLICATION NUMBER: US/09/955,732  
; CURRENT FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-732-3

Query Match 100.0%; Score 52; DB 9; Length 156;

Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 97 VHCLAGISRS 106

## RESULT 15

US-09-955-732-4

; Sequence 4, Application US/09955732  
; Publication No. US20020182203A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.433  
; CURRENT APPLICATION NUMBER: US/09/955,732  
; CURRENT FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-955-732-4

Query Match 100.0%; Score 52; DB 9; Length 156;

Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 97 VHCLAGISRS 106

## RESULT 16

US-10-346-356-13

; Sequence 13, Application US/10346356  
; Publication No. US20030138931A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.416C1  
; CURRENT APPLICATION NUMBER: US/10/346,356

; CURRENT FILING DATE: 2003-01-15  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-346-356-13

Query Match 100.0%; Score 52; DB 14; Length 167;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 108 VHCLAGISRS 117

## RESULT 17

US-09-775-925-24

; Sequence 24, Application US/09775925  
; Patent No. US20010049358A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY  
; TITLE OF INVENTION: PHOSPHATASES  
; FILE REFERENCE: 200125.420  
; CURRENT APPLICATION NUMBER: US/09/775,925  
; CURRENT FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-775-925-24

Query Match 100.0%; Score 52; DB 9; Length 168;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 108 VHCLAGISRS 117

## RESULT 18

US-09-847-519A-9

; Sequence 9, Application US/09847519A  
; Patent No. US20020102693A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.422  
; CURRENT APPLICATION NUMBER: US/09/847,519A  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-519A-9

Query Match 100.0%; Score 52; DB 9; Length 168;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
| | | | | | | | | |  
Db 108 VHCLAGISRS 117

```
RESULT 19
US-10-314-058-13
; Sequence 13, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-13
Query Match 100.0%; Score 52; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 108 VHCLAGISRS 117

RESULT 20
US-10-405-808-15
; Sequence 15, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1
; CURRENT APPLICATION NUMBER: US/10/405,808
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-405-808-15
Query Match 100.0%; Score 52; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 108 VHCLAGISRS 117

RESULT 21
US-10-655-073-15
; Sequence 15, Application US/10655073
; Publication No. US20040043411A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418C1
; CURRENT APPLICATION NUMBER: US/10/655,073
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-655-073-15
Query Match 100.0%; Score 52; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 108 VHCLAGISRS 117

RESULT 22
US-10-962-126-24
; Sequence 24, Application US/10962126
; Publication No. US20050058650A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.420C1
; CURRENT APPLICATION NUMBER: US/10/962,126
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 09/775,925
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 60/179,886
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-962-126-24
Query Match 100.0%; Score 52; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 108 VHCLAGISRS 117

RESULT 23
US-10-644-554-16
; Sequence 16, Application US/10644554
; Publication No. US20050075489A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413C1
; CURRENT APPLICATION NUMBER: US/10/644,554
; CURRENT FILING DATE: 2003-08-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-644-554-16
Query Match 100.0%; Score 52; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
Db 108 VHCLAGISRS 117
```



```
RESULT 24
US-10-658-661-12
; Sequence 12, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.408C2
; CURRENT APPLICATION NUMBER: US/10/658,661
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-661-12
Query Match 100.0%; Score 52; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 108 VHCLAGISRS 117

RESULT 25
US-10-346-356-12
; Sequence 12, Application US/10346356
; Publication No. US20030138931A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416C1
; CURRENT APPLICATION NUMBER: US/10/346,356
; CURRENT FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-356-12
Query Match 100.0%; Score 52; DB 14; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 110 VHCLAGISRS 119

RESULT 26
US-10-346-356-15
; Sequence 15, Application US/10346356
; Publication No. US20030138931A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416C1
; CURRENT APPLICATION NUMBER: US/10/346,356
; CURRENT FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 169
; TYPE: PRT
US-10-346-356-15
Query Match 100.0%; Score 52; DB 14; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 110 VHCLAGISRS 119

RESULT 27
US-09-775-925-23
; Sequence 23, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-23
Query Match 100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 110 VHCLAGISRS 119

RESULT 28
US-09-775-925-26
; Sequence 26, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY
; FILE REFERENCE: 200125.420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-925-26
Query Match 100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10
| | | | | | | |
Db 110 VHCLAGISRS 119

RESULT 29
US-09-847-519A-8
; Sequence 8, Application US/09847519A
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; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.422
; CURRENT APPLICATION NUMBER: US/09/847,519A
; CURRENT FILING DATE: 2001-05-01
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-8

Query Match      100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 30
US-09-847-519A-11
; Sequence 11, Application US/09847519A
; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.422
; CURRENT APPLICATION NUMBER: US/09/847,519A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-11

Query Match      100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 30
US-09-847-519A-11
; Sequence 11, Application US/09847519A
; Patent No. US20020102693A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.422
; CURRENT APPLICATION NUMBER: US/09/847,519A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-11

Query Match      100.0%; Score 52; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 31
US-10-314-058-12
; Sequence 12, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-12

Query Match      100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 31
US-10-314-058-12
; Sequence 12, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-12

Query Match      100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 32
US-10-314-058-14
; Sequence 14, Application US/10314058
; Publication No. US20030119045A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415C1
; CURRENT APPLICATION NUMBER: US/10/314,058
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-314-058-14

Query Match      100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 33
US-10-405-808-14
; Sequence 14, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1
; CURRENT APPLICATION NUMBER: US/10/405,808
; CURRENT FILING DATE: 2003-04-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-405-808-14

Query Match      100.0%; Score 52; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 34
US-10-405-808-16
; Sequence 16, Application US/10405808
; Publication No. US20030175829A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-4 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.410C1
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; CURRENT APPLICATION NUMBER: US/10/405,808  
 ; CURRENT FILING DATE: 2003-04-01  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16  
 ; LENGTH: 170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-405-808-16

Query Match 100.0%; Score 52; DB 14; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 Db 110 VHCLAGISRS 119

RESULT 35  
 US-10-655-073-14  
 ; Sequence 14, Application US/10655073  
 ; Publication No. US20040043411A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luche, Ralf M.  
 ; APPLICANT: Wei, Bo  
 ; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE  
 ; FILE REFERENCE: 200125.418C1  
 ; CURRENT APPLICATION NUMBER: US/10/655,073  
 ; CURRENT FILING DATE: 2003-09-04  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 14  
 ; LENGTH: 170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-655-073-14

Query Match 100.0%; Score 52; DB 15; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 Db 110 VHCLAGISRS 119

RESULT 36  
 US-10-655-073-16  
 ; Sequence 16, Application US/10655073  
 ; Publication No. US20040043411A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luche, Ralf M.  
 ; APPLICANT: Wei, Bo  
 ; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE  
 ; FILE REFERENCE: 200125.418C1  
 ; CURRENT APPLICATION NUMBER: US/10/655,073  
 ; CURRENT FILING DATE: 2003-09-04  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16  
 ; LENGTH: 170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-655-073-16

Query Match 100.0%; Score 52; DB 15; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 Db 110 VHCLAGISRS 119

RESULT 37  
 US-10-962-126-23  
 ; Sequence 23, Application US/10962126  
 ; Publication No. US20050058650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luche, Ralf M.  
 ; APPLICANT: Wei, Bo  
 ; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY  
 ; TITLE OF INVENTION: PHOSPHATASES  
 ; FILE REFERENCE: 200125.420C1  
 ; CURRENT APPLICATION NUMBER: US/10/962,126  
 ; CURRENT FILING DATE: 2004-10-08  
 ; PRIOR APPLICATION NUMBER: US 09/775,925  
 ; PRIOR FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: US 60/179,886  
 ; PRIOR FILING DATE: 2000-02-02  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-962-126-23

Query Match 100.0%; Score 52; DB 17; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 Db 110 VHCLAGISRS 119

RESULT 38  
 US-10-962-126-26  
 ; Sequence 26, Application US/10962126  
 ; Publication No. US20050058650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luche, Ralf M.  
 ; APPLICANT: Wei, Bo  
 ; TITLE OF INVENTION: DSP-12 AND DSP-13 DUAL-SPECIFICITY  
 ; TITLE OF INVENTION: PHOSPHATASES  
 ; FILE REFERENCE: 200125.420C1  
 ; CURRENT APPLICATION NUMBER: US/10/962,126  
 ; CURRENT FILING DATE: 2004-10-08  
 ; PRIOR APPLICATION NUMBER: US 09/775,925  
 ; PRIOR FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: US 60/179,886  
 ; PRIOR FILING DATE: 2000-02-02  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 26  
 ; LENGTH: 170  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-962-126-26

Query Match 100.0%; Score 52; DB 17; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VHCLAGISRS 10  
 Db 110 VHCLAGISRS 119

RESULT 39  
 US-10-644-554-15  
 ; Sequence 15, Application US/10644554  
 ; Publication No. US20050075489A1  
 ; GENERAL INFORMATION:

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; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413C1
; CURRENT APPLICATION NUMBER: US/10/644,554
; CURRENT FILING DATE: 2003-08-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-644-554-15

Query Match      100.0%; Score 52; DB 17; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 40
US-10-644-554-17
; Sequence 17, Application US/10644554
; Publication No. US20050075489A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413C1
; CURRENT APPLICATION NUMBER: US/10/644,554
; CURRENT FILING DATE: 2003-08-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-644-554-17

Query Match      100.0%; Score 52; DB 17; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 41
US-10-658-661-11
; Sequence 11, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.408C2
; CURRENT APPLICATION NUMBER: US/10/658,661
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-658-661-11

Query Match      100.0%; Score 52; DB 18; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 42
US-10-658-661-13
; Sequence 13, Application US/10658661
; Publication No. US20050176124A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-3 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.408C2
; CURRENT APPLICATION NUMBER: US/10/658,661
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-658-661-13

Query Match      100.0%; Score 52; DB 18; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      110 VHCLAGISRS 119

RESULT 43
US-09-925-299-842
; Sequence 842, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 842
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-842

Query Match      100.0%; Score 52; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VHCLAGISRS 10
Db      99 VHCLAGISRS 108

RESULT 44
US-09-925-299-842
; Sequence 842, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
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; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 842
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-842

Query Match      100.0%; Score 52; DB 10; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      99 VHCLAGISRS 108

RESULT 45
US-10-029-345A-191
; Sequence 191, Application US/10029345A
; Publication No. US20050130286A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
; FILE REFERENCE: D0072.NP
; CURRENT APPLICATION NUMBER: US/10/029,345A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/256,868
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 60/280,186
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/287,735
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 60/295,848
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/300,465
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-345A-191

Query Match      100.0%; Score 52; DB 18; Length 302;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VHCLAGISRS 10
Db      242 VHCLAGISRS 251

Search completed: August 31, 2005, 11:14:15
Job time : 161 secs
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2005, 02:00:40 ; Search time 2061 Seconds  
(without alignments)  
10587.567 Million cell updates/sec

Title: US-09-964-277-20

Perfect score: 3332

Sequence: 1 gagagaagagagataata.....ataagatgaacttggttc 3332

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 733684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

; Maximum Match 100%

; Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	3332	100.0	3332	9	US-09-964-277-20
2	3158	94.8	3496	9	US-09-964-277-1
3	3145	94.4	3625	18	US-10-425-114-26234
4	3133.4	94.0	3521	20	US-10-370-715B-261
5	3118.8	93.6	3766	18	US-10-343-357-17
6	3106.2	93.2	5450	22	US-10-029-345A-108
7	3106.2	93.2	5450	22	US-10-029-345A-147
					Sequence 20, Appli
					Sequence 1, Appli
					Sequence 26234, A
					Sequence 261, App
					Sequence 17, Appl
					Sequence 108, App
					Sequence 147, App

8	2950	88.5	3544	9	US-09-816-494-1	Sequence 1, Appli
9	2950	88.5	3544	17	US-10-377-072-25	Sequence 25, Appl
10	2950	88.5	3544	19	US-10-377-072-25	Sequence 25, Appl
11	2950	88.5	5145	20	US-10-357-930-20824	Sequence 20824, A
12	2950	88.5	5145	20	US-10-357-930-20969	Sequence 20969, A
13	2950	88.5	5145	20	US-10-357-930-21071	Sequence 21071, A
14	2950	88.5	5145	20	US-10-357-930-21083	Sequence 21083, A
15	2950	88.5	5145	20	US-10-357-930-21303	Sequence 21303, A
16	2950	88.5	5145	20	US-10-357-930-21307	Sequence 21307, A
17	2950	88.5	5145	20	US-10-357-930-22820	Sequence 22820, A
18	2950	88.5	5145	20	US-10-357-930-26669	Sequence 26669, A
19	2950	88.5	5145	20	US-10-357-930-26815	Sequence 26815, A
20	2950	88.5	5145	20	US-10-357-930-26923	Sequence 26923, A
21	2950	88.5	5145	20	US-10-357-930-27145	Sequence 27145, A
22	2950	88.5	5145	20	US-10-357-930-27149	Sequence 27149, A
23	2950	88.5	5145	20	US-10-357-930-28675	Sequence 28675, A
24	2950	88.5	5111	22	US-10-029-345A-41	Sequence 41, Appl
25	2924.6	87.8	4790	19	US-10-648-593-115	Sequence 115, App
26	2766.4	83.0	3059	18	US-10-257-026-1	Sequence 1, Appli
27	2710	81.3	2966	18	US-10-296-115-520	Sequence 520, App
28	2602.8	78.1	2732	18	US-10-168-506-2	Sequence 2, Appli
29	2390.8	71.8	2732	21	US-10-838-181-2	Sequence 2, Appli
30	2390.8	71.8	2732	21	US-10-108-260A-2429	Sequence 2429, Ap
31	1795.4	53.9	1916	17	US-10-094-749-673	Sequence 673, App
32	1762.4	52.9	2102	17	US-10-072-012-255	Sequence 255, App
33	1742	52.3	2200	18	US-10-072-012-257	Sequence 257, App
34	1712.4	51.4	2071	18	US-10-072-012-257	Sequence 3, Appli
35	1660	49.8	1998	9	US-09-816-494-3	Sequence 27, Appl
36	1660	49.8	1998	17	US-10-377-072-27	Sequence 27, Appl
37	1660	49.8	1998	19	US-10-377-072-27	Sequence 113, App
38	1638.2	49.2	2756	22	US-10-029-345A-113	Sequence 1750, Ap
39	886.8	26.6	2558	17	US-10-104-047-1750	Sequence 85, Appl
40	595	17.9	787	17	US-10-220-891-85	Sequence 158, App
41	537.4	16.1	877	9	US-09-764-853-158	Sequence 10717, A
42	417.2	12.5	425	20	US-10-357-930-10717	Sequence 31909, A
43	415.2	12.5	467	20	US-10-357-930-31909	Sequence 40868, A
44	415.2	12.5	467	20	US-10-357-930-40868	Sequence 41017, A
45	415.2	12.5	467	20	US-10-357-930-41017	

#### ALIGNMENTS

#### RESULT 1

US-09-964-277-20  
; Sequence 20, Application US/09964277  
; Patent No. US2002013170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.434  
; CURRENT APPLICATION NUMBER: US/09/964,277  
; CURRENT FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 3332  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-277-20

Query Match 100.0%; Score 3332; DB 9; Length 3332;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	GCAGAGCGGAGCGCAGCGCCCTCTCGGCTCCGCGCGCGCTCCGAGTCCGGAGGC	120

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QY 181 GTCCGGGGCCCAAAAGCTTTCACTCCAGTGTAAAGCTGTGAGAGCGCGGAGCAAAAGGT 240  
DB 181 GTCCGGGGCCCAAAAGCTTTCACTCCAGTGTAAAGCTGTGAGAGCGCGGAGCAAAAGGT 240  
QY 241 AAAGAAATGATTAATCGCTGGCTCCAAAGCATCTTTTGTGTGGAAATGGTTATTC 300  
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QY 301 AGTCATCTCTTTAATGAAATCAAAATGTGAGGGGTGCTTTGTGACGAGTCCCTTTGCAAGA 360  
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QY 421 TAACTCTCTTTTCCAGTCACCAACAGCTGACCTCATACACTTTTGTAGTACAAATGGAGT 480  
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DB 481 GGCTGAGCCTTTGAGCACACCACTTACATCATCTGCGCAAAATTAAGAGAGAGGTGG 540  
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DB 781 AAACATAAGGTTGACATTTGATTCAGTCAAGAGTTGTAGTTTACGATCAAAAGCTCCCAA 840  
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DB 1741 TCAGGAACTATCGGAGCAGACTCCCGAAACCACTCTGATAGGAGGAGCAGCATCC 1800  
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DB 1861 AACAGCAGAGTGGACCGCCAGAGTCCCTTTTATCTCCACTGCTATCGAAGTGGAG 1920  
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DB 1921 CGTGAGGACAAATACCAACAGCTTCTTTTCGGCCCTTCCACAGCCAGCAGCACCT 1980  
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DB 1981 CACGAAGCTGTGCGCCCTGGGCTTTAAGGGCTGGCACTCGGATATCTTTGGCCCCCAGAC 2040  
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DB 2041 CTCTACCCCTTCCCTGACAGCAGCTGGTATTTTGGCAGAGTCTCTACACTTCTACTC 2100  
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DB 2101 TGCCCTCAGCCATCTACGAGGAGCGCACTTCTGCTACAGCTGCGAGCAGCTGCC 2160  
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DB 2221 CTCGCGGGGAGCTGGCATGAAGAGAGCCCTTTTGAAGAGCTTTTAAACGAGAGCTG 2280  
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Db	781	AAACATAAGGTTGACATGATGATGACAGTTCAGAAAGTTGTAGTTTACATCAAAAGCTCCCAA	840
QY	841	GATGTTGCCCTCTCTCTTCAGACTGTTTCTCAGTACTCTGAGTACTCTGGTAAACTGGAGAAG	900
Db	841	GATGTTGCCCTCTCTCTTCAGACTGTTTCTCAGTACTCTGAGTACTCTGGTAAACTGGAGAAG	900
QY	901	AGCTTCAAACTCTGTTCACTGCTTTCG	926
Db	901	AGCTTCAAACTCTGTTCACTGCTTTCGAGTGGGTTTGCTGAGTTCCTCTGTTGTTCCCT	960
QY	927	-----	926
Db	961	GGCCTCTGTGAAGGAAATCCACTAGTCCCTACCTGCATTTCTCAGGCTTGCTTTACCT	1020
QY	927	-----	926
Db	1021	GTTCGCCAACTTGGGCCAACCCGAAATTCCTCCAAATCTTTATCTTGGCTGCCAGCGAGAT	1080
QY	927	-----AGGAGCTGATGCAGCAGAAATGGGATTTGTTATGTTTAAATGCCAGCAAT	976
Db	1081	GTCTCMAAAGAGGCTGATGCAGCAGAAATGGGATTTGTTATGTTTAAATGCCAGCAAT	1140
QY	977	ACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGTGTGCTGTGGAATGAC	1036
Db	1141	ACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGCTGTGCTGTGGAATGAC	1200
QY	1037	AGCTTTGTGAGAAATTTTGGCGTGTGGAATAATCAGTAGATTTTCAATTGAGGAAGCA	1096
Db	1201	AGCTTTGTGAGAAATTTTGGCGTGTGGAATAATCAGTAGATTTTCAATTGAGGAAGCA	1260
QY	1097	AAAGCCTCCAAATGGATGTGTTCTAGTGCACTGTGTTAGCTGGGATCTCCCGCTCCGCCACC	1156
Db	1261	AAAGCCTCCAAATGGATGTGTTCTAGTGCACTGTGTTAGCTGGGATCTCCCGCTCCGCCACC	1320
QY	1157	ATCGCTATCGCTACATCATGAAAGAGATGGACATGTTTATGATGAAAGCTTACAGATTT	1380
Db	1321	ATCGCTATCGCTACATCATGAAAGAGATGGACATGTTTATGATGAAAGCTTACAGATTT	1380
QY	1217	GTGAAGAAAGAGCTACTATATCTCCAAATCTCAATTTCTGGGCCAACTCTCTGGAC	1276
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QY	1337	CTGCACCTGGAGAGCCAAATGAACTGTCCTGCTGTCTCAGAGGGTGGACAGAAAGC	1396
Db	1501	CTGCACCTGGAGAGCCAAATGAACTGTCCTGCTGTCTCAGAGGGTGGACAGAAAGC	1560
QY	1397	GAGAGCCCTCAGTCCACCCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGCAAAAGG	1456
Db	1561	GAGAGCCCTCAGTCCACCCCTGTGCCGACTCTGCTACCTCAGAGGCAGCAGCAAAAGG	1620
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Db	1621	CCCGTGCATCCCGCCAGCTGCCAGCGTGCAGCGTGCAGCGCTCGCTGTTAGAGGAC	1680
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Db	1681	AGCCCGCTGTGTACAGGCGCTCAGTGGGCTGCACTGTCCGACAGCAGGCTGGAGAAGCAGC	1740
QY	1577	AATAGCTCAAGCGTTCCTCTCTCTGGATATCAATCAGTTCATATTCAGCCAGCATG	1636
Db	1741	AATAGCTCAAGCGTTCCTCTCTCTGGATATCAATCAGTTCATATTCAGCCAGCATG	1800
QY	1637	GCAGCATCCTTACATGGCTTCTCTCATCAGAGATGCTTTGGAATACTACAAACCTTCC	1696
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Db	1861	ACTACTCTGGATGGAGCAACCAAGCTATGCCCAGTTCTCCCTGTTCAGGAACTATCGGAG	1920
QY	1757	CAGACTCCCGAAACCAAGTCTTGATAAGGAGGAAGCCAGCATCCCAAGAAAGCTGCAGACC	1816
Db	1921	CAGACTCCCGAAACCAAGTCTTGATAAGGAGGAAGCCAGCATCCCAAGAAAGCTGCAGACC	1980
QY	1817	GCCAGGCTTTCAGACAGCCAGAGCAAGGATTTGCAATTCGGTTCAGAACCAAGCAGCAGTGCG	1876
Db	1981	GCCAGGCTTTCAGACAGCCAGAGCAAGGATTTGCAATTCGGTTCAGAACCAAGCAGCAGTGCG	2040
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Db	2041	ACCGCCAGAGGTCCTTTTATCTCCACTGCAATGAGTGGGAGCGTGGAGGACAAATAC	2100
QY	1937	CACACAGCTTCTTTTGGGCTTTCCACCCAGCAGCAGCACTCACGAAGTCTGCTGGC	1996
Db	2101	CACACAGCTTCTTTTGGGCTTTCCACCCAGCAGCAGCACTCACGAAGTCTGCTGGC	2160
QY	1997	CTGGGCTTTAAGGCTGCGACTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTG	2056
Db	2161	CTGGGCTTTAAGGCTGCGACTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTG	2220
QY	2057	ACCAGCAGCTGATTTTGGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTAC	2116
Db	2221	ACCAGCAGCTGATTTTGGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCATCTAC	2280
QY	2117	GGAGGCACTGCGCAGTTCCTCTGCTACAGCTGCAGCAGCTGCCCACTTTCGCGAGACCAA	2176
Db	2281	GGAGGCACTGCGCAGTTCCTCTGCTACAGCTGCAGCAGCTGCCCACTTTCGCGAGACCAA	2340
QY	2177	GTCTATTCCTGCGCAGGCGCAGAAAGCAAGTGAAGAGTGACTCGCGGCGGAGCTGG	2236
Db	2341	GTCTATTCCTGCGCAGGCGCAGAAAGCAAGTGAAGAGTGACTCGCGGCGGAGCTGG	2400
QY	2237	CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACCCAGAGCTGCCAAATGGAATTTGA	2296
Db	2401	CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACCCAGAGCTGCCAAATGGAATTTGA	2460
QY	2297	GAGAGCATCATCTCAGAGAAACAGGTTCACGGGAAGAGCTGGGAAAAGTGGGCACTCT	2356
Db	2461	GAGAGCATCATCTCAGAGAAACAGGTTCACGGGAAGAGCTGGGAAAAGTGGGCACTCT	2520
QY	2357	AGCTTTTGGGCGAGCATGGAATTCATGAGTCTCTCTGAGAAAGAAAGACACTTGTGACTT	2416
Db	2521	AGCTTTTGGGCGAGCATGGAATTCATGAGTCTCTCTGAGAAAGAAAGACACTTGTGACTT	2580
QY	2417	CTATAGACAAATTTTCTTCTGTTTTCACAAAATAATTCCTCTGTAATCTGAAATATATAT	2476
Db	2581	CTATAGACAAATTTTCTTCTGTTTTCACAAAATAATTCCTCTGTAATCTGAAATATATAT	2640
QY	2477	ATGTACATACATATATATTTTGGAAAATGGAGCTATGTTGTAATAAGCAACAGGTGGATC	2536
Db	2641	ATGTACATACATATATATTTTGGAAAATGGAGCTATGTTGTAATAAGCAACAGGTGGATC	2700
QY	2537	AACCCAGTTGTTTACTCTCTTAAACATCTGCAATTTGAGAGATTCAGCTAATCTCTCTCAAC	2596
Db	2701	AACCCAGTTGTTTACTCTCTTAAACATCTGCAATTTGAGAGATTCAGCTAATCTCTCTCAAC	2760
QY	2597	AAAAATGGAGGCGCAGATCTAGAAATCCCCCTAGACGGGAGGAAACCAATTTTATTCAGT	2656
Db	2761	AAAAATGGAGGCGCAGATCTAGAAATCCCCCTAGACGGGAGGAAACCAATTTTATTCAGT	2820
QY	2657	GAATTACACATCTCTTGTCTTTAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAAATC	2716
Db	2821	GAATTACACATCTCTTGTCTTTAAAAAGCAAGTGTCTTTGGTGTGGAGGACAAAATC	2880
QY	2717	CCCTACCATTTTCCAGCTTGTGCTACTAGAGATCTCAATATATTAGTCTTTGTCCGACC	2776
Db	2881	CCCTACCATTTTCCAGCTTGTGCTACTAGAGATCTCAATATATTAGTCTTTGTCCGACC	2940
QY	2777	CTTCCATAGTACACCTTTAGCGCTGAGACTGAGCCAGCTTTGGGGGTTCAGGTAGTAGACCC	2836

2941 CTTCCATAGTACACCTTAGAGCTGAGACTGAGCAGCTTGGGGTTCAGTGTAGTAGACC 3000  
 2837 TGTTAGGACAGAGCTAGTGTAAATCAAGAGAAATGATCCTATCCAAAGCTGATTCA 2896  
 3001 TGTTAGGACAGAGCTAGTGTAAATCAAGAGAAATGATCCTATCCAAAGCTGATTCA 3060  
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 3421 TACCTCCCTCTTTGTAATCAAGAAATTTTAAATGGGATTTGCAATCCTTTAAATAA 3480  
 3317 AGATGAACCTTGGTTTC 3332  
 3481 AGATGAACCTTGGTTTC 3496

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 ; Sequence 26234, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 26234  
 ; LENGTH: 3625  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB4119-028-H6\_FLI  
 US-10-425-114-26234

Query Match 94.4%; Score 3145; DB 18; Length 3625;  
 Best Local Similarity 95.3%; Pred. No. 0;  
 Matches 3330; Conservative 0; Mismatches 0; Indels 165; Gaps 2;  
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62 CGAGCGGAGCGCAGCGCCCTCTCGGCTCCGGCGCGCGCTCGCAAGTCCGGGAGGCG 121  
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 122 AGGGGCGCGGAGCGCGTGTGACAACTTTGTTTCCCTCTGAGGGAATTTGGGAGG 181  
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 362 CACATCAACGGGAAAGAGAGACATTTCACTTTGGAGGGCTCTTGTGAAAATTTGGGTTT 421  
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 612 GCTGAGCTTTGAGCAGCAGCAGCAGTATCATCTGCGCAATTTAAGAGAGGAGTGGGA 671  
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 902 GCTTCAACTCTGTTCACTGCTTGC----- 926  
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 927 -----AGAGCTGATGAGGAGATGGATTTGTTTATGTGTAAATGCCAGCAATA 977  
 1212 TCCTCAACAGAGGCTGATGAGGAGATGGATTTGTTTATGTGTAAATGCCAGCAATA 1271  
 978 CTTGTCCAAAGCGCTGACTTTTATCCCGGAGTCTCAATTTCTCGGTGTGCTGTGAATGACA 1037

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1038	Qy	GCCTTTTGTGAGAAAAATTTTCGCGTGGTGTGACAAAATCAGTAGAATTTTCATTGTGAAAAAGCAA	1097
1332	Db	GCCTTTTGTGAGAAAAATTTTCGCGTGGTGTGACAAAATCAGTAGAATTTTCATTGTGAAAAAGCAA	1391
1098	Qy	AAGCCTCCAATGGATGTGTTCTTAGTGCACTGTGTTTAGCTGGGATCTCCCGCTCGCCACCA	1157
1392	Db	AAGCCTCCAATGGATGTGTTCTAGTGCACTGTGTTTAGCTGGGATCTCCCGCTCGCCACCA	1451
1158	Qy	TGCGTATCGGCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTTG	1217
1452	Db	TGCGTATCGGCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTTTG	1511
1218	Qy	TGAAGAAAAAAGACCTACTATATCTCCAACCTTCAATTTTCTGGGCGCAACTCCTCGACT	1277
1512	Db	TGAAGAAAAAAGACCTACTATATCTCCAACCTTCAATTTTCTGGGCGCAACTCCTCGACT	1571
1278	Qy	ATGAGAAAGAGATTAAAGAACCGAGACTGGAGCATCAGGGCCAAAAGAGCAAACTCAAGCTGC	1337
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1338	Qy	TGCACCTTGGAGAAAGCCAAAATGAACCTGTCCCTGTCTGTCTCAGAGGGTGGACAGAAAGCG	1397
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1398	Qy	AGACGCCCTCAGTGCACACCTGTGCGCACTCTGTCTACTCTCAGAGGCGACGAGCAAGGC	1457
1692	Db	AGACGCCCTCAGTGCACACCTGTGCGCACTCTGTCTACTCTCAGAGGCGACGAGCAAGGC	1751
1458	Qy	CCGTGCATCCCGCCAGCGTGCACCGTGCACCGTGCACCGTGCCTGTGTAGAGGACA	1517
1752	Db	CCGTGCATCCCGCCAGCGTGCACCGTGCACCGTGCACCGTGCCTGTGTAGAGGACA	1811
1518	Qy	GCCCGCTGGTACAGCGGCTCAGTGGGGTGCACCTGTCCGAGACAGGCTCGAAACAGACA	1577
1812	Db	GCCCGCTGGTACAGCGGCTCAGTGGGGTGCACCTGTCCGAGACAGGCTCGAAACAGACA	1871
1578	Qy	ATAAGCTCAAGCGTTCCTTCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGG	1637
1872	Db	ATAAGCTCAAGCGTTCCTTCTCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGG	1931
1638	Qy	CAGCATCCTTACATGGCTTCCTCTCATCAGAAGATGCTTTTGGAAATCTACAAACCTTTCCA	1697
1932	Db	CAGCATCCTTACATGGCTTCCTCTCATCAGAAGATGCTTTTGGAAATCTACAAACCTTTCCA	1991
1698	Qy	CTACTCTGGATGGGACCAACAAAGCTATGCCAGTTTCTCCCTGTTCAGGAATCTATCGGAGC	1757
1992	Db	CTACTCTGGATGGGACCAACAAAGCTATGCCAGTTTCTCCCTGTTCAGGAATCTATCGGAGC	2051
1758	Qy	AGACTCCGGAACAGTCTCTGATTAAGAGGAGAGCCAGCATCCCCAAGAGCTGCAGACCG	1817
2052	Db	AGACTCCGGAACAGTCTCTGATTAAGAGGAGAGCCAGCATCCCCAAGAGCTGCAGACCG	2111
1818	Qy	CCAGSCCTTCAGACAGCCAGAGCAAGCGATTGCAATTCGTTTCAGAAACAGAGAGTGGCA	1877
2112	Db	CCAGSCCTTCAGACAGCCAGAGCAAGCGATTGCAATTCGTTTCAGAAACAGAGAGTGGCA	2171
1878	Qy	CCGCCCCAGAGTCCCTTTTATCTCCACTGCAATCGAAGTGGGAGCGTGGAGGACAATTTACC	1937
2172	Db	CCGCCCCAGAGTCCCTTTTATCTCCACTGCAATCGAAGTGGGAGCGTGGAGGACAATTTACC	2231
1938	Qy	ACAACAGCTTCCTTTTCTGGGCTTTTCCACAGCGAGCAGCACTCAGAGAGTCTCTCGGCC	1997
2232	Db	ACAACAGCTTCCTTTTCTGGGCTTTTCCACAGCGAGCAGCACTCAGAGAGTCTCTCGGCC	2291
1998	Qy	TGGGCTTTAAGGGCTGGCACTCGGATATCTTTGGGCCCCCGAGACCTCTACCCCTTCCCTGA	2057
2292	Db	TGGGCTTTAAGGGCTGGCACTCGGATATCTTTGGGCCCCCGAGACCTCTACCCCTTCCCTGA	2351
2058	Qy	CCAGCAGCTGTGATTTTGGCCACAGAGTCTCACACTTCTACTCTGCGCTCAGGCCACTTACG	2117

2352	DB	CGAGCAGCTGGTAATTTTGGCCACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACG	2411
2118	QY	GAGCGAGTGCAGTTACTCTGCCCTACAGCTGCAGCCAGCTGCCACCTTGGGAGACCAAG	2177
2412	DB	GAGCGAGTGCAGTTACTCTGCCCTACAGCTGCAGCCAGCTGCCACCTTGGGAGACCAAG	2471
2178	QY	TCTATTCTGTGCGGAGCGGCAGAACGCAAGTGCACAGAGCTGACTCGCGCGGAGCTGGC	2237
2472	DB	TCTATTCTGTGCGGAGCGGCAGAACGCAAGTGCACAGAGCTGACTCGCGCGGAGCTGGC	2531
2238	QY	ATGAGGAGAGCCCTCTTGAAGACAGTTTAAACGCGAGAGCTGCCAAATCGAAATTTGGAG	2297
2532	DB	ATGAGGAGAGCCCTCTTGAAGACAGTTTAAACGCGAGAGCTGCCAAATCGAAATTTGGAG	2591
2298	QY	AGAGCATCATGTTCAGAGAAACAGGTCACGGGAAGAGCTGGGAAAGTGGGCAGTCAGTCTA	2357
2592	DB	AGAGCATCATGTTCAGAGAAACAGGTCACGGGAAGAGCTGGGAAAGTGGGCAGTCAGTCTA	2651
2358	QY	GCCTTTTCGGGAGCATGGAAATCATTTGAGGTCCTCTGAGAGAAAGACACTTTGTGACTTC	2417
2652	DB	GCCTTTTCGGGAGCATGGAAATCATTTGAGGTCCTCTGAGAGAAAGACACTTTGTGACTTC	2711
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2772	DB	TGTACATACATATATATTTTTTGGAAATGAGGCTATGGTGTAAAGCAACAGGTTGATCA	2831
2538	QY	ACCAGTTGTACTCTCTTAACATCTGCAATTTGAGAGATCAGCTAATATCTTCTCAACA	2597
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2952	DB	AAATPACATCTCTCTGTCTTAAAGCAAGTGTCTTTGGTGTTCGGAGCAAAAATCC	3011
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3012	DB	CCTACCAATTTT-CACGTTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCGGACCC	3070
2778	QY	TTCCATAGTACACCTTAGCCGTGAGACTGAGCCAGCTTGGGGGTTCAGGTAGGTAGACCT	2837
3071	DB	TTCCATAGTACACCTTAGCCGTGAGACTGAGCCAGCTTGGGGGTTCAGGTAGGTAGACCT	3130
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3191	DB	AAACCCACGCTCACCTGACAGCCGAGGGAACGAGCATCACTCTGTGGACGGACCAATTA	3250
2958	QY	GGGGCCTTCCAAAGGTCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAGTGGGGC	3017
3251	DB	GGGGCCTTCCAAAGGTCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAGTGGGGC	3310
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3311	DB	TTTGACCACTACCATATCTGTAGCCCATTTTCTAGGCATTTGTGAATAGGTAGGTAGCTA	3370
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3371	DB	GTCACACTTTTCAGACCAATTCAAACTGTCTATGCACAAAATTCCTCGTGGCCCTAGATGG	3430
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QY 2741 ACTAAGAGATCTCAAAATATTAGTCTTGTCCGACCCCTTCCATAGTACACCTTAGCCGCTG 2800  
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Db 2940 AGACTGAGCCAGCTTGGGGGTTCAGGTAGTAGAGCCCTGTTAGGACAGAGCTTAGTGTA 2999  
QY 2861 AATCCAAAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCAGCTCAGCTGACAGCC 2920  
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QY 3161 CTTTATGAAGAGAGGAAACTGTCTAGGATTCAGCTGAACCCAGGAACTCTGGCAACA 3220  
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QY 3281 AATTGTTTAAATCGGATTTGCAATCTTTTAAATAAAGATCAACTTGGTTTC 3332  
Db 3420 AATTGTTTAAATCGGATTTGCAATCTTTTAAATAAAGATCAACTTGGTTTC 3471

## RESULT 6

US-10-029-345A-108  
; Sequence 108, Application US/10029345A  
; Publication No. US20050130286A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES  
; FILE REFERENCE: D0072 NP  
; CURRENT APPLICATION NUMBER: US/10/029,345A  
; PRIORITY FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/256,868  
; PRIORITY FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 60/280,186  
; PRIORITY FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/287,735  
; PRIORITY FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 60/295,848  
; PRIORITY FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/300,465  
; PRIORITY FILING DATE: 2001-06-25  
; NUMBER OF SEQ ID NOS: 208



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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 5450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (538)..(2532)
US-10-029-345A-108

Query Match      93.2%; Score 3106.2; DB 22; Length 5450;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 3304; Conservative 3; Mismatches 3; Indels 166; Gaps 3;

QY 25  GAAAGAGAGGAGGAGAGAGCGACGCGACGCGAGCGGAGCGGAGCGCGCCCTC 84
DB 1  GAAAGAGAGGAGGAGAGAGCGACGCGAGCGGAGCGGAGCGGAGCGCGCCCTC 60

QY 85  TCGGCTCCGCGCGCGCCCTCGCAAGTCCGGAGGCGAGGGGGGCCGAGGGGAGACGCC 144
DB 61  TCGGCTCCGCGCGCGCCCTCGCAAGTCCGGAGGCGAGGGGGGCCGAGGGGAGACGCC 120

QY 145  GTGACAACTTTCCTTCCCTCTGAGGGAATTGGGGAATTCGGCGGCCCAAAAGCTTTCAG 204
DB 121  GTGACAACTTTCCTTCCCTCTGAGGGAATTGGGGAATTCGGCGGCCCAAAAGCTTTCAG 180

QY 205  TCCAGTGAAGCTGTGGAGCGCGGAGCAAGGTAAAGATGATGTAATGCGCTGGCT 264
DB 181  TCCAGTGAAGCTGTGGAGCGCGGAGCAAGGTAAAGATGATGTAATGCGCTGGCT 240

QY 265  GCTCCAAAGCATCTTTTGTGGAAATGGTTAATCCAGTCATCTCTTTAATGAATCAAAATG 324
DB 241  GCTCCAAAGCATCTTTTGTGGAAATGGTTAATCCAGTCATCTCTTTAATGAATCAAAATG 300

QY 325  TGAGGGGCTGCTTTGTGAGCGGAGTCTTTGCAAGAGCAATCAAGCGGAAAGAGAAAGA 384
DB 301  TGAGGGGCTGCTTTGTGAGCGGAGTCTTTGCAAGAGCAATCAAGCGGAAAGAGAAAGA 360

QY 385  GACATTCACCTTGAGGGCTCTGCTGAAAATGGTTTAAGTCTCTTTTGGCAGTCACCA 444
DB 361  GACATTCACCTTGAGGGCTCTGCTGAAAATGGTTTAAGTCTCTTTTGGCAGTCACCA 420

QY 445  CCAGCTGACCTCATACACTTTTAGTACAAATGAGTGGCTGAGCCTTTGAGCACACACC 504
DB 421  CCAGCTGACCTCATACACTTTTAGTACAAATGAGTGGCTGAGCCTTTGAGCACACACC 480

QY 505  ATTCATCATCTGCTGGCAAAATTAAGAGGAGGTGGGAAAGAGGACTTAATGTTGTCATG 564
DB 481  ATTCATCATCTGCTGGCAAAATTAAGAGGAGGTGGGAAAGAGGACTTAATGTTGTCATG 540

QY 565  GCCCATGAGATGATGGAACCTCAAAATGTTTACTGAGAGGTGGTGGCTCTGCTGGAAGT 624
DB 541  GCCCATGAGATGATGGAACCTCAAAATGTTTACTGAGAGGTGGTGGCTCTGCTGGAAGT 600

QY 625  GGAACGGAAGAGTGTCTGCTAAATGATGAGCGGCCAATTTGTGGAATACATAATCCAC 684
DB 601  GGAACGGAAGAGTGTCTGCTAAATGATGAGCGGCCAATTTGTGGAATACATAATCCAC 660

QY 685  ATTTTGGAGCCATTAAATATCAACTGCTCCAAAGCTTATGAAGCGAAGGTTGCAACAGGAC 744
DB 661  ATTTTGGAGCCATTAAATATCAACTGCTCCAAAGCTTATGAAGCGAAGGTTGCAACAGGAC 720

QY 745  AAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGTTGACATGATTGC 804
DB 721  AAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAAACATAAGTTGACATGATTGC 780

QY 805  AGTCAGAGGTGTAGTTTACGATCAAGCTCCCAAGATGTGCTCTCTCTCTTCAGAC 864
DB 781  AGTCAGAGGTGTAGTTTACGATCAAGCTCCCAAGATGTGCTCTCTCTCTTCAGAC 840

QY 865  TGTCTTCTCACTGTACTTCTGGGTAAACTGGAGAGAGCTTCAACTCTGTTCACCTGCTT 924
DB 841  TGTCTTCTCACTGTACTTCTGGGTAAACTGGAGAGAGCTTCAACTCTGTTCACCTGCTT 900

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QY 925  GC----- 926
DB 901  GCAGTGGTTTGTCTAGTCTCTCTGTTGTTTCCCTGGCCTCTGTGAAGAAAAATCCACT 960
QY 927  ----- 926
DB 961  CTAGTCCCTACCTGCAATTTCTCAGCCTTGTCTTACCTGTGGCAACATTTGGGCAACCCGA 1020
QY 927  -----AGGAGCTGATGAG 940
DB 1021  ATTCTTCCCAATCTTTATCTTTGGCTGCCAGCGAGATGTCTCAACAAGAGAGCTGATACAG 1080
QY 941  CAGAAATGGATTTGTTATGTTAAATGCCAGCAATACCTGTCTCAAAGCCCTGACTTTATC 1000
DB 1081  CAGAAATGGATTTGTTATGTTAAATGCCAGCTATACCTGTCTCAAAGCCCTGACTTTATC 1140
QY 1001  CCGAGTCTCATCTTCCCTGCGGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCG 1060
DB 1141  CCGAGTCTCATCTTCCCTGCGGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCG 1200
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DB 1201  TGGTTGGACAAATCAGTAGATTTTCAATTCAGAAAGCAAAAGCCCTCAATGGATGTGTTCTA 1260
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DB 1261  GTGCACTGTTTAGCTGGGATCTCCGCTCCGCAACCATCGCTATCGCTATCATCATGAAG 1320
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DB 1321  AGGATGACATGTCCTTTAGATGAGCTTACAGATTTGTGAAGAAAAAGACCTACTATA 1380
QY 1241  TCTCCAAACTTCAATTTTCTGGGCCAACTCTCTGGACTATGAGAGAAAGATTAAGAACCCAG 1300
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DB 1561  GCGGACTCTGTCTACCTCAGAGGACAGCAAGAGCCGCTGCATCCCGCCAGCGGTGCC 1620
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DB 1621  AGCGTGCCCGAGCGTGCAGCCGCTGTGTAGAGGACAGCCCGCTGTGTACAGGCGCTCAGT 1680
QY 1541  GGGCTGCACCTGTCTCGCAGACAGGCTGGAGAGCAGCAATAAGCTCAAGCGTTCCTCTCT 1600
DB 1681  GGGCTGCACCTGTCTCGCAGACAGGCTGGAGAGCAGCAATAAGCTCAAGCGTTCCTCTCT 1740
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DB 1741  CTGGATATCAAAATCAGTTTTCATATTTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCC 1800
QY 1661  TCATCAGAAAGATGCTTTTGAATATCTACAAACCTTCCACTTCTTGGATGGGACCAACAAG 1720
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QY 1721  CTATGCCAGTCTCCCTCTGTTTCCAGGAACTATTCGAGAGACATCCCGAAACCGAGTCTGAT 1780
DB 1861  CTATGCCAGTCTCCCTCTGTTTCCAGGAACTATTCGAGAGACATCCCGAAACCGAGTCTGAT 1920
QY 1781  AAGGAGGAAGCCAGCATCCCAAGAGCTGAGAGCCGAGCCGCTTTCAGACAGCCAGAGC 1840
DB 1921  AAGGAGGAAGCCAGCATCCCAAGAGCTGAGAGCCGAGCCGCTTTCAGACAGCCAGAGC 1980

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Db 121 GTGCAAACTTTTCCTCTGAGGGAATTGGAGGTGGCGGCCCAAAAGCTTTTCAG 180  
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Db 181 TCCAGTGAAGACTGTTGGAGCGCGGAGCAAGCTAAAGATGATGTAATGCGCTGGCT 240  
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Db 241 GCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCAGTCACTCTTTTATGAATCAAAATG 300  
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Db 301 TGAGGGGCTGCTTTGTGAGCGAGTCTTTTGAAGAGCACATCAAGCGGAAGAGAGA 360  
Qy 385 GACATTCACCTGAGGGCTCTTCTGAAATGGTTTAACTCTCTCTTTGCGCAGTCACCA 444  
Db 361 GACATTCACCTGAGGGCTCTTCTGAAATGGTTTAACTCTCTCTTTGCGCAGTCACCA 420  
Qy 445 CCAGGCTGACCTCATACACTTTTAGTACAAATGGAGTGGCTGAGCCCTTTGAGCACACCACC 504  
Db 421 CCAGGCTGACCTCATACACTTTTAGTACAAATGGAGTGGCTGAGCCCTTTGAGCACACCACC 480  
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Db 481 ATTACATCATCTGGCAAAATTAAGAGAGAGTGGGAAAGAGACTTATTTGTTGTCATG 540  
Qy 565 GCCCATGAGATGATGGAACCTCAAAATGTTTACTGAGAGGTTGGTGGCTCTGCTGGAAGT 624  
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Qy 685 ATTTGGAAAGCATTAATATCAATCACTGCTCCAGCTTTAAGACGGAAGGTTGCAACAGAC 744  
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Db 841 TGTTTTCTCACTGTACTCTGGGTAACTGGGAGAGACTTCAACTCTGTTCACTGCTTT 900  
Qy 925 GC----- 926  
Db 901 GCAGGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGGCTCTGTGGAAGAAATCCACT 960  
Qy 927 ----- 926  
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Db 1861 CTATGCAAGTGTCTCCCTGTTTCAGGAATCTTCGGAGCAGACTCCCGAAACAGTCTGAT 1920  
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Db 1921 AAGGAGGAGCCAGCATCCCAAGAGCTGCAGACCGCCAGCCCTTCAGACAGCCAGAGC 1980  
Qy 1841 AAGCGATTTGCAATTCGGTTCAGAAACCAAGCAGCAGTGGCACCGCCAGAGGTCCTTTTATCT 1900  
Db 1981 AAGCGATTTGCAATTCGGTTCAGAAACCAAGCAGCAGTGGCACCGCCAGAGGTCCTTTTATCT 2040  
Qy 1901 CCACTGCAATGCAAGTGGGAGCGTGGAGGACAAATTAACCAACAGGTTCTTTTTCGGCTTT 1960  
Db 2041 CCACTGCAATGCAAGTGGGAGCGTGGAGGACAAATTAACCAACAGGTTCTTTTTCGGCTTT 2100  
Qy 1961 TCCACAGCCAGCAGCAGCTCAAGAGTCTGCTGGCCCTTAAAGGCTGGCACTCG 2020  
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Db 2161 GATATCTTTGGCCCCCAGACCTCTTACCCTTCCCTGACAGCAGCTGGTATTTTGGCCACA 2220  
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Db 2221 GAGTCTTCACTTCTACTCTGCTTCAGCCATCTACGAGGAGTTCAGAGTACTCTGCC 2280  
Qy 2141 TACAGTGGAGCCAGCTGCCCACTTTCGGAGACCAAGTCTATTTCTGTCGAGGGGGCAG 2200  
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Db 3103 TGACAGCGAGGACACGAGCATCACTCTGCTGGACGGACCATTAGGGGCTTGCACAGG 3162
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Db 3163 TCTACTCTTAGACAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222
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RESULT 9
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-0180NM1
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419

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; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25

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Query Match 88.5%; Score 2950; DB 17; Length 3544;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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3273 AATCAAGAAATTTGTTTTAAATGGGATTTGTAATCTCTTTTAAATGAAGATGAATCTGTTTC 3332

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RESULT 11
US-10-357-930-20824
; Sequence 20824, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20824
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

Query Match 88.5%; Score 2950; DB 20; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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Db 224 GCTTTTCAGTCCAGTGTAAGCTGTTGGAGCGCGGAGCAAGGTAAAGATGATGTAATG 283
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QY 257 CGCTGCTGCTCCAAAGCATCTTTGTTGGAATGGTTATTCAGTCACTCTTTTATGA 316
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QY 917 ACCTGCTTGC----- 926
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RESULT 12

US-10-357-20969  
; Sequence 20969, Application US/10357930  
; Publication No. US2004025908A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endege, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314

Qy	927	-----	926
Db	1004	AA <sup>1</sup> PC <sup>2</sup> ACTCTAG <sup>3</sup> CCCT <sup>4</sup> ACTGCT <sup>5</sup> ATTTCTCAGCCTTGC <sup>6</sup> TTTACTGTTG <sup>7</sup> CCAA <sup>8</sup> CA <sup>9</sup> AT <sup>10</sup> TGGC <sup>11</sup>	1063
Qy	927	-----	AGGAGC 932
Db	1064	CA <sup>1</sup> ACC <sup>2</sup> CGA <sup>3</sup> ATTCTTCC <sup>4</sup> AA <sup>5</sup> TCTTTATCTTGGCTG <sup>6</sup> CCAGCGAGATG <sup>7</sup> TCTCTCA <sup>8</sup> CAAGAGC <sup>9</sup>	1123
Qy	933	TGATG <sup>1</sup> CAGCAGA <sup>2</sup> ATGGG <sup>3</sup> ATTG <sup>4</sup> TATGTGTTAAATGCCAGCAATAC <sup>5</sup> CTGTCCAAAGCCTG <sup>6</sup>	992
Db	1124	TGATG <sup>1</sup> CAGCAGA <sup>2</sup> ATGGG <sup>3</sup> ATTG <sup>4</sup> TATGTGTTAAATGCCAGCAATAC <sup>5</sup> CTGTCCAAAGCCTG <sup>6</sup>	1183
Qy	993	ACTTTAT <sup>1</sup> CCCGAG <sup>2</sup> CTCAT <sup>3</sup> TTCTCGGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA	1052
Db	1184	ACTTTAT <sup>1</sup> CCCGAG <sup>2</sup> CTCAT <sup>3</sup> TTCTCGGTGTGCCTGTGAATGACAGCTTTTGTGAGAAAA	1243
Qy	1053	TTTTGGCGTGG <sup>1</sup> TGGACAAATCAGT <sup>2</sup> AGATTCTTCAATGGAAGCAAAAGCCCTCCAATCGAT	1112
Db	1244	TTTTGGCGTGG <sup>1</sup> TGGACAAATCAGT <sup>2</sup> AGATTCTTCAATGGAAGCAAAAGCCCTCCAATCGAT	1303
Qy	1113	GTG <sup>1</sup> TTCTAGTGC <sup>2</sup> ACTGTTT <sup>3</sup> AGCTGGGATCTCCCGCTCCGACCATCGCTATCGCCTACA	1172
Db	1304	GTG <sup>1</sup> TTCTAGTGC <sup>2</sup> ACTGTTT <sup>3</sup> AGCTGGGATCTCCCGCTCCGACCATCGCTATCGCCTACA	1363
Qy	1173	TCATGAAGAGGATGG <sup>1</sup> ACATGCTCTTT <sup>2</sup> ATAGTGAAGCTTACAGATTGTTGAAGAAAAAGAC	1232
Db	1364	TCATGAAGAGGATGG <sup>1</sup> ACATGCTCTTT <sup>2</sup> ATAGTGAAGCTTACAGATTGTTGAAGAAAAAGAC	1423
Qy	1233	CTACTATATCTCCAAACTTCAA <sup>1</sup> TTTTCTGGGCGCAACTCTCGGTGGACTATGAGAGAAGATTA	1292
Db	1424	CTACTATATCTCCAAACTTCAA <sup>1</sup> TTTTCTGGGCGCAACTCTCGGTGGACTATGAGAGAAGATTA	1483
Qy	1293	AGAACAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTCGAGAGAC	1352
Db	1484	AGAACAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTCGAGAGAC	1543
Qy	1353	CAAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAGCGAGACGCCCCCTCAGTC	1412
Db	1544	CAAAATGAACCTGTCCCTGTGCTCTCAGAGGGTGGACAGAAAGCGAGACGCCCCCTCAGTC	1603
Qy	1413	CACCTGTGCCGACTCTGCTTACCTCAGAGCAGCAGACAGAAAGCCCGTGCATCCCGCCA	1472
Db	1604	CACCTGTGCCGACTCTGCTTACCTCAGAGCAGCAGACAGAAAGCCCGTGCATCCCGCCA	1663
Qy	1473	CGGTGCCAGCGTGCCAGCGTGCAGCGCTCGCTGTTTAGAGGACAGCCCGCTGCTACAGG	1532
Db	1664	CGGTGCCAGCGTGCCAGCGTGCAGCGCTCGCTGTTTAGAGGACAGCCCGCTGCTACAGG	1723
Qy	1533	CGCTCAGTGGGCTGCACCTGTCCGACAGAGGCTGGGAAGACAGCAATAAGCTCAAGCGTT	1592
Db	1724	CGCTCAGTGGGCTGCACCTGTCCGACAGAGGCTGGGAAGACAGCAATAAGCTCAAGCGTT	1783
Qy	1593	CTTTCTCTTGGAATACAAATCAGTTTCATATTACGCGAGCATGGGAGCATCTCTTACATG	1652
Db	1784	CTTTCTCTCTTGGAATACAAATCAGTTTCATATTACGCGAGCATGGGAGCATCTCTTACATG	1843
Qy	1653	GC <sup>1</sup> TTCTCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTCGATGGGA	1712
Db	1844	GC <sup>1</sup> TTCTCTCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCCACTACTCTCGATGGGA	1903
Qy	1713	CCAAACAGCTATGCCAGTTCTCCCTGTTCAGGAACTATCGGAGCAGATCTCCGAAACCA	1772
Db	1904	CCAAACAGCTATGCCAGTTCTCCCTGTTCAGGAACTATCGGAGCAGATCTCCGAAACCA	196
Qy	1773	GTCCTGATTAAGAGGAAGCCAGCATCCCAAGAAAGCTGCGACCGCCAGGCTTTCAGACA	1833
Db	1964	GTCCTGATTAAGAGGAAGCCAGCATCCCAAGAAAGCTGCGACCGCCAGGCTTTCAGACA	202
Qy	1833	GCCAGACAGCGGATTCGATTCGCTCAGAACCCAGCAGTGGCCACCGCCAGAGGTCCTC	1899
Db	2024	GCCAGACAGCGGATTCGATTCGCTCAGAACCCAGCAGTGGCCACCGCCAGAGGTCCTC	208
Qy	1893	TTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTTACCAACAGAGTTCCTTT	195

Db 2084 TTTTATCTCCATGCAATGAAAGTGGAGCGTGGAGCAAAATACACACCCAGCTTCCTTT 2143  
QY 1953 TCGGCTTTTCCACGACGACGACCTCAGCAAGTCTGCTGGCGCTGGGCTTTAAGGCT 2012  
Db 2144 TCGGCTTTTCCACGACGACGACCTCAGCAAGTCTGCTGGCGCTGGGCTTTAAGGCT 2203  
QY 2013 GGCACCTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGTAAT 2072  
Db 2204 GGCACCTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTGACCCAGCAGCTGTAAT 2263  
QY 2073 TTGCCACAGAGCTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGCAGTGCAGTT 2132  
Db 2264 TTGCCACAGAGCTCTCACACTTCTACTCTGCTCAGCCATCTACGGAGCAGTGCAGTT 2323  
QY 2133 ACTCTGCTTACAGCTGCAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGCA 2192  
Db 2324 ACTCTGCTTACAGCTGCAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGCGCA 2383  
QY 2193 GCGGCGAGAGCCAACTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCT 2252  
Db 2384 GCGGCGAGAGCCAACTGACAGAGCTGACTCGCGGCGGAGCTGGCATGAAGAGAGCCCT 2443  
QY 2253 TTGAAAGCAGTTTAAACGACAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTGAG 2312  
Db 2444 TTGAAAGCAGTTTAAACGACAGAGCTGCCAAATGGAATTTGGAGAGCATCATGTGAG 2503  
QY 2313 AGAACAGGTACGCGGAGAGCTGGGGAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 2372  
Db 2504 AGAACAGGTACGCGGAGAGCTGGGGAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 2563  
QY 2373 TGGAAATCATTTGAGTCTCTGAGAGAAAGACACTTTGTGACTTCTATAGACAAATTTTT 2432  
Db 2564 TGGAAATCATTTGAGTCTCTGAGAGAAAGACACTTTGTGACTTCTATAGACAAATTTTT 2623  
QY 2433 TTTCTTTGTTTACAAAAAATTCCTCTGTAATCTGAAATATATATATATATATATATATAT 2492  
Db 2624 TTTCTTTGTTTACAAAAAATTCCTCTGTAATCTGAAATATATATATATATATATATATAT 2683  
QY 2493 ATTTTGGAAATGGAGCTATGTTGTAAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 2552  
Db 2684 ATTTTGGAAATGGAGCTATGTTGTAAGCAAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 2743  
QY 2553 TCTTAACATCTGATTTGAGAGTACGCTAAATCTCTCAACAAAAATGGAAGGCGAG 2612  
Db 2744 TCTTAACATCTGATTTGAGAGTACGCTAAATCTCTCAACAAAAATGGAAGGCGAG 2803  
QY 2613 ATGCTAGAATCCCTCTAGACGGAGGAAAAACCAATTTTATTCAGTGAATTACACATCCTCT 2672  
Db 2804 ATGCTAGAATCCCTCTAGACGGAGGAAAAACCAATTTTATTCAGTGAATTACACATCCTCT 2863  
QY 2673 TGTTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAAATCCCTACCATTTTCCAC 2732  
Db 2864 TGTTCTTAAAAAGCAAGTGTCTTTGGTGTGGAGACAAAAATCCCTACCATTTT-CAC 2922  
QY 2733 GTTGTGCTACTAGAGTCTCAATATTAGTCTTTCTCGGACCTTCCATAGTACACCT 2792  
Db 2923 GTTGTGCTACTAGAGTCTCAATATTAGTCTTTCTCGGACCTTCCATAGTACACCT 2982  
QY 2793 TAGGCTTGAGCTGAGCCAGCTTTGGGGTTCAGGTAGTACACCTTGTAGGGACAGAGCC 2852  
Db 2983 TAGGCTTGAGCTGAGCCAGCTTTGGGGTTCAGGTAGTACACCTTGTAGGGACAGAGCC 3042  
QY 2853 TAGTGTGTAATCCAAAGAAATGATCTATCCAAAGCTGATTCACAAAACCCAGCTCACC 2912  
Db 3043 TAGTGTGTAATCCAAAGAAATGATCTATCCAAAGCTGATTCACAAAACCCAGCTCACC 3102  
QY 2913 TGCAGCGGAGGACAGCAGCATCACTCTCTGAGCGGACCAATAGGGGCTTGGCAAG 2972  
Db 3103 TGCAGCGGAGGACAGCAGCATCACTCTCTGAGCGGACCAATAGGGGCTTGGCAAG 3162  
QY 2973 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTGGGGCTTTTGACCACTACCAT 3032

Db 3163 TCTACCTTAGAGCAAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCAT 3222  
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Db 3223 ATCTGGTAGCCATTTTCTAGGCATTTGGAATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3282  
QY 3093 CCAATTCAACTGTCTATGCAAAAAATCCCGTGGGCTAGATGGAGATAATTTTTTTTTT 3152  
Db 3283 CCAATTCAACTGTCTATGCAAAAAATCCCGTGGGCTAGATGGAGATAATTTTTTTTTT 3342  
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Db 3343 CTTCTCAGCTTTTGAAGAGAGGAAACTGTCTAGGATTCAGCTGAAACCAACCAGGAACC 3402  
QY 3213 TGGCAACATCAGATTTAAGCTTAAGCTTGGAGGCTAACCGAGTCTACCTCCTCTTTGTA 3272  
Db 3403 TGGCAACATCAGATTTAAGCTTAAGCTTGGAGGCTAACCGAGTCTACCTCCTCTTTGTA 3462  
QY 3273 AATCAAGAAATGTTTAAATGGGATTTGTCATCTTTTAAATTAAGATGAACCTTGGTTTC 3332  
Db 3463 AATCAAGAAATGTTTAAATGGGATTTGTCATCTTTTAAATTAAGATGAACCTTGGTTTC 3522

RESULT 13  
US-10-357-930-21071  
; Sequence 21071, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endege, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21071  
; LENGTH: 5145  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1, 5144, 5145  
; OTHER INFORMATION: n = A,T,C or G  
US-10-357-930-21071

Query Match 88.5%; Score 2950; DB 20; Length 5145;  
Best Local Similarity 95.0%; Pred. No. 0;  
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;  
QY 197 GCTTTTCAGTCCAGTGTAAAGCTGTGGAGCGCGGAGCAAAAGGTAAGAATGATGTAATG 256  
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QY 257 CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATTCAGTCTATCTTTATCA 316

Db 284 CGCTGGCTGCTCCAAAGCACTCTTTGTTGTGGAAATGGTTATTTCCAGTCATCTCTTTATGA 343  
Qy 317 ATCAAAATGTAGGGGCTGCTTTGTGGACGGAGTCCTTTTGCAGAGCACATCAACGGGAAA 376  
Db 344 ATCAAAATGTAGGGGCTGCTTTGTGGACGGAGTCCTTTTGCAGAGCACATCAACGGGAAA 403  
Qy 377 GAGAAAGAGACATTCACCTTGGAGGGCTCTTGTGAAATGGTTTAACTCTCTCTTTTGGC 436  
Db 404 GAGAAAGAGACATTCACCTTGGAGGGCTCTTGTGAAATGGTTTAACTCTCTCTTTTGGC 463  
Qy 437 AGTCACCAACGAGCTGACCTCATACATTTTGTAGTACAAATGGAGTGGCTTGTAGC 496  
Db 464 AGTCACCAACGAGCTGACCTCATACATTTTGTAGTACAAATGGAGTGGCTTGTAGC 523  
Qy 497 ACACCAACATTCATCATCTGTGGCAAAATTAAGAAAGGAGGTGGGAAAAAGAGACTTATTG 556  
Db 524 ACACCAACATTCATCATCTGTGGCAAAATTAAGAAAGGAGGTGGGAAAAAGAGACTTATTG 583  
Qy 557 TTGTCTATGGCCCATGAGATGATTTGGAACCTCAAAATTTTACTGAGAGGTTGGTCTTGC 616  
Db 584 TTGTCTATGGCCCATGAGATGATTTGGAACCTCAAAATTTTACTGAGAGGTTGGTCTTGC 643  
Qy 617 TGGAAAGTGGAAACGGAAGGCTGCTAAATTTGATAGCGGCCATTTGTGGAATACAATA 676  
Db 644 TGGAAAGTGGAAACGGAAGGCTGCTAAATTTGATAGCGGCCATTTGTGGAATACAATA 703  
Qy 677 CATCCACATTTTGGAGCCATTAATATCAACTGCTTCCAAAGCTTATGAAGCGAAGGTTGC 736  
Db 704 CATCCACATTTTGGAGCCATTAATATCAACTGCTTCCAAAGCTTATGAAGCGAAGGTTGC 763  
Qy 737 AACAGGAAAGGTTTAATACAGAGCTCATCCAGCATTCAGCAACATTAAGGTTGACA 796  
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Qy 797 TTGATTGCACTCAGAGGTTGTAGTTTACGATCAAGCTCCCAAGATTTGCTCTCTCT 856  
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Qy 857 CTTGAGACTGTTTTCTCACTGACTCTCGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC 916  
Db 884 CTTGAGACTGTTTTCTCACTGACTCTCGGGTAAACTGGAGAGAGCTTCAACTCTGTTTC 943  
Qy 917 ACTGCTTGC----- 926  
Db 944 ACTGCTTGCAGGTGGGTTTGTGAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGGAA 1003  
Qy 927 ----- 926  
Db 1004 AATCCACTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACTGTTGCCAATTTGGC 1063  
Qy 927 -----AGGAGC 932  
Db 1064 CAACCGAATTTCTCCCAATCTTTATCTTTGGCTGCGCAGGAGATGTCTCAACAGGAGC 1123  
Qy 933 TGATGACAGAGATGGGATTTGTTATGTTTAAATGCCAGCAATACCTGTCCAAGCCTG 992  
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Qy 1113 GTGTTCTAGTGCACTGTTTAGCTGGGATCTCCGCTCCGCCACCATCGTATCGCTACA 1172  
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Db 1364 TCATGAAGAGGATGGACATGTTCTTTTAGATGAAGCTTTACAGATTTGTGAAAGAAAAAGAC 1423

Qy 1233 CTACTATATCTCAAACCTTCAATTTTCTGGCCAACTCCTCGACTATGAGAAGAGATT 1292  
Db 1424 CTACTATATCTCAAACCTTCAATTTTCTGGCCAACTCCTCGACTATGAGAAGAGATT 1483  
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Qy 1353 CAAATGAACCTGTCTCTGCTGTCTCAGAGGCTGACAGAAAAGAGAGCGCCCTCTAGTC 1412  
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Db 1604 CACCTGTGCGGACTCTGCTTACCTCAGAGGAGCAGAGCAAAAGGCGGTGATCCCGCA 1663  
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Qy 1653 GCTTCTCTCATCAGAGATGCTTTTGGAACTACTACAAACCTTCCACTACTCTGGATGGGA 1712  
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Qy 1713 CCAACAGCTATGCGAGTTCTCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1772  
Db 1904 CCAACAGCTATGCGAGTTCTCCCTGTTCAGGAACTATCGGAGCAGACTCCCGAAACCA 1963  
Qy 1773 GTCTGTATAGGAGGAGCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 1832  
Db 1964 GTCTGTATAGGAGGAGCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTTCAGACA 2023  
Qy 1833 GCCAGAGCAAGCGATTGCAATTCGGTTCAGAACAGCAGCAGTGGCACCCGCCAGAGGTCCC 1892  
Db 2024 GCCAGAGCAAGCGATTGCAATTCGGTTCAGAACAGCAGCAGTGGCACCCGCCAGAGGTCCC 2083  
Qy 1893 TTTTATCTCCATCGAATCGGAGCTGGAGGACAAATTAACAACAGCTTTCCTTT 1952  
Db 2084 TTTTATCTCCATCGAATCGGAGCTGGAGGACAAATTAACAACAGCTTTCCTTT 2143  
Qy 1953 TCGGCTTTCCACGAGCAGCAGCACTTCAGAACTGCTGCTGGCTGGGCTTAAGGGCT 2012  
Db 2144 TCGGCTTTCCACGAGCAGCAGCACTTCAGAACTGCTGCTGGCTGGGCTTAAGGGCT 2203  
Qy 2013 GGCACTCGGATATCTTGGCCCCCAGAGCTCTACCCCTTCCCTGACACAGCAGCTGGTATT 2072  
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Qy 2133 ACTGCTCTACAGCTGAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGGCA 2192  
Db 2324 ACTGCTCTACAGCTGAGCAGCTGCCACTTGGGAGACCAAGTCTATTCTGTGGCA 2383  
Qy 2193 GGCGCAAGCAGCAGTGCAGAGCTGACTCGCGCGGAGCTGGCATCAAGAGAGCCCT 2252  
Db 2384 GGCGCAAGCAGCAGTGCAGAGCTGACTCGCGCGGAGCTGGCATCAAGAGAGCCCT 2443  
Qy 2253 TTGAAAAGCAGTTTAAACGCAAGAGCTGCCAAATGGAAATTTTGGAGAGAGCATCATGTGAG 2312  
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QY 2733 GTTGTGCTACTAGAGATCTCAAAATATTAGTCTTTGTCCGGACCCCTCCATAGTACACT 2792
Db 2923 GTGTGCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGGACCCCTCCATAGTACACT 2982
QY 2793 TAGCGCTGAGCTGAGCCAGCTTGGGGGTACAGTGTAGAGCCCTGTAGGACAGAGCC 2852
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Db 3043 TAGTGGTAAATCAAGAGAAATGATCTTATCCAAAGCTGATTCACAAACCCACGCTCACC 3102
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QY 3093 CCAATTCAAACTGTCTATCCACAAATTCCTCGTGGCCCTAGATGGAGATAATTTTTTTT 3152
Db 3283 CCAATTCAAACTGTCTATCCACAAATTCCTCGTGGCCCTAGATGGAGATAATTTTTTTT 3342
QY 3153 CTCTCAGCTTTATGAAGAGAGGAAACTGTCTAGGATTCAGCTGAAACCCAGGAAAC 3212
Db 3343 CTCTCAGCTTTATGAAGAGAGGAAACTGTCTAGGATTCAGCTGAAACCCAGGAAAC 3402
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Db 3403 TGGCAACATCAGATTTAAGCTTAAGTTGGGAGGCTAAGAGTCTACCTCCCTCTTTGTA 3462
QY 3273 AATCAAGATTTGTTTAAATGGGATTTCAATCCCTTTAAATAAAGATGAATGTTGTTTC 3332
Db 3463 AATCAAGATTTGTTTAAATGGGATTTGTCATTCCTTTTAAATAAAGATGAATGTTGTTTC 3522
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## RESULT 15

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US-10-357-930-21303
; Sequence 21303, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21303
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; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21303
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Query Match 88.5%; Score 2950; DB 20; Length 5145;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 3135; Conservative 0; Mismatches 0; Indels 165; Gaps 2;

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.434  
; CURRENT APPLICATION NUMBER: US/09/964,277  
; CURRENT FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 3332  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-964-277-20

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy 361 ValGluAspLeuTyrHisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeu 380
Db 1922 GTGAGAGCAATATACCAACACAGCTTCTTTTCGGCCCTTCCACAGCCAGCAGCACCTC 1981

Qy 381 ThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThr 400
Db 1982 ACGAAGTCTGCTGGCCTGGGCTTAAGGGCTGGGCACTCGGATATCTTGGCCCCCAGACC 2041

Qy 401 SerThrProSerLeuThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSer 420
Db 2042 TCTACCCCTTCCCTGACCCAGCAGCTGGTATTTTGGCCACAGAGTCTCTCACACTTCTACTCT 2101

Qy 421 AlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuPro 440
Db 2102 GCCTCAGCCATCTACGAGGAGGCGCCAGTTACTTCTGCCTACAGCTGCAGCGCTGCC 2161

Qy 441 ThrCysGlyAspGlnValTyrSerValArgArgArgGlnLysProSerAspArgAlaAsp 460
Db 2162 ACTTGGGAGACCAAGTCTATTCTGTGCGAGCGCGGAGAGCCAGTGCAGAGCTGAC 2221

Qy 461 SerArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSerCys 480
Db 2222 TCGCGCGAGCTGGCATGAAGAGAGCGCCCTTTCAAAAGCAGTTTAAACGCGAGAAGCTGC 2281

Qy 481 GlnMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluLeuGlyLys 500
Db 2282 CAATATGGAATTTGAGAGAGCATCATGTACAGAAACAGGTCAAGGAGAGCTGGGAGAA 2341

Qy 501 ValGlySerGlnSerSerPheSerGlySerMetGluIleLeuGluValSer 517
Db 2342 GTGGCAGCTCAGTCTAGCTTTTCGGGCGAGCATGGAAATCATTTAGGTCTCC 2392
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## RESULT 2

US-09-816-494-3  
; Sequence 3, Application US/09816494  
; Patent No. US20020034807A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel A.  
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY  
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR  
; FILE REFERENCE: 10448-030002  
; CURRENT APPLICATION NUMBER: US/09/816,494  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 60/191,858  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1998  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-816-494-3

Alignment Scores:  
Pred. No.: 4, 43e-251 Length: 1998  
Score: 2606.00 Matches: 516  
Percent Similarity: 90.21% Conservative: 0  
Best Local Similarity: 90.21% Mismatches: 1  
Query Match: 97.68% Indels: 56  
DB: 9 Gaps: 1

US-09-964-277-21 (1-517) x US-09-816-494-3 (1-1998)

Qy 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20  
Db 281 ATGTTGCGCTCTCTCTCTCAGACTGTTTCTCAGTGTACTTCTGGTAAACTGGGAAGA 340  
Qy 21 AlaserThrLeuPheThrCysLeuGln-----29  
Db 341 GCTTCAACTCTGTTCACTGCTTGCA-GGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCT 399  
Qy 29 -----29  
Db 400 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 459  
Qy 29 -----29  
Db 460 GTTGCAACATNTGGGCCAACCGAATCTTCCCAATCTTTATCTTGGCTGCCAGCAGAT 519  
Qy 30 -----GlulMetGlnGlnAenGlyIleGlyTyrValLeuAsnAlaSerAsn 45  
Db 520 GTTCCTCAACAGAGCTGATGAGCAGAAATGGATTTGGTTATGTGTAAATGCCAGCAAT 579  
Qy 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65  
Db 580 ACTGTGCCAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGAC 639  
Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85  
Db 640 AGCTTTTGTGAGAAATTTGCGGTGTGGCAATCAGTAGATTTTCATTGAGAAAGCA 699  
Qy 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105  
Db 700 AAGCCTCAATGGATGTTCTTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACC 759  
Qy 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125  
Db 760 ATCGCTATCGCTACATCATGATGAAGAGTGGACATGTCTTTAGATCAAGCTTTACAGATTT 819  
Qy 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAsp 145  
Db 820 GTGAAAGAAAGAACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGAC 879  
Qy 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLysLeu 165  
Db 880 TATGAGAGAGATTAAGAACACAGCTGGAGATCAGGGCCCAAGAGCAACTCAAGCTG 939  
Qy 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185  
Db 940 CTGCACCTGGAGAAGCAAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGC 999  
Qy 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArg 205  
Db 1000 GAGACGCCCTCAGTCCACCTGTGCGGACTCTGTCTACCTCAGAGCAGCAGCAAGG 1059  
Qy 206 ProValHisProAlaSerValProSerValGlnProSerLeuGlnLeuGluAsp 225  
Db 1060 CCGTGCATCCCCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGT 1119  
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Db 1120 AGCCCCGTGTACAGCGCTCAGTGGCTGCACCTGTCCGACAGAGCTGGGAAGACAGC 1179  
Qy 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265  
Db 1180 AATAAGCTCAAGCGTTCTCTCTCTGATATCAAAATCAGTTTTCATATTCAGCCAGCATG 1239  
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Db 1300 ACTACTCTGGATGGGACCAACAGCTATGCCAGTTCTCCCTGTTTCCAGGAACCTATCGGAG 1359

Qy 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325  
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Db 1540 CACACAGCTCTCTTTTCGGCTTTCACACAGCAGCAGCACCTCAGCAAGTCTGCTGGC 1599  
Qy 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405  
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Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445  
Db 1720 GGAGCAGTCCAGTTACTCTGCTTACAGCTGCAGCAGCTGCCACTTGGCGAGACCAA 1779  
Qy 446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgSerTrp 465  
Db 1780 GTCTATTCTGTGCGCGCGCAGAGCAAGTGCAGAGCTGACTCTCGCGCGGAGCTGG 1839  
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Db 1840 CATGAGAGAGCCCTTTGAAAGCAGTTTAAACGAGAAGCTGCCAATGGAATTGGA 1899  
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RESULT 3  
US-10-377-072-27  
; Sequence 27, Application US/10377072  
; Publication No. US20040009501A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Glucksman, Maria A.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Williamson, Mark J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Chun, Miyoung  
; APPLICANT: Tsai, Fong-Ying  
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,  
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MPI03-0180NMIM  
; CURRENT APPLICATION NUMBER: US/10/377,072  
; CURRENT FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: US 09/895,860  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215,370  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/723,806  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,455  
; PRIOR FILING DATE: 2000-03-07

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; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 4,43e-251 Length: 1998
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 17 Gaps: 1

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db 281 ATGTTGGCTCTCTCTTCAGACTGTTTCTCAGTACTTCTGCTGTTAACTGGAGAAGA 340
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 341 GCTTCAACTCTGTTCACTGCTGTGCA-GGTGGGTTTGTGAGTTCTCTCGTTGTTCCCT 399
QY 29 ----- 29
Db 400 GGCCTCTGTGAAGGAAATCCACTAGTCCCTACCTGATTTCTCAGCCTTGCTTACCT 459
QY 29 ----- 29
Db 460 GTTGCCACATTGGGCCAACCGAATCTTCCCAATCTTATCTTTGGCTGCCAGCGAGAT 519
QY 30 -----GlueuMetGlnGlnAsnGlylleGlyTyrValLeuAsnAlaSerAsn 45
Db 520 GTCCCTCAACAGGAGCTGATGCAGCAGAATGGGATGGTTATGTTGTTAAATGCCAGCAAT 579
QY 46 ThrCysProLysProAspPheileProGluSerHisPheLeuArgValProValAsnAsp 65
Db 580 ACCTGTCCAAAGCCGTGACTTTATCCCGAGTCTCATTTCTCGGTGCTGCTGTAATGAC 639
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheilleGluLysAla 85
Db 640 AGCTTTTGTGAGAAATTTTGGCGTGGTTGGACAATCAGTAGATTTTCATTGAGAAAGCA 699
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 700 AAAGCCTCCAAATGGATGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 759
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 760 ATCGCTATCGCCTACATCATGAAGAGGATGGACATGTTCTTTAGATGAAGCTTACAGATT 819
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
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QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db 940 CTGCACCTTGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAGC 999
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1000 GAGAGCCCCCTCAGTCCACCTGTGCCGACTCTCTACCTCAGAGGAGCAGGAGCAAGG 1059
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuAsp 225
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QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1120 AGCCCGCTGGTACAGGGCGCTCAGTGGCTGCACCTGTCCGACAGAGGCTGGAGACAGC 1179
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Db 1240 GCAGCATCCTTACATGGCTTCTCTCATCAGAAAGATGCTTTGGAATACTACAAACCTTCC 1299
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Db 1780 GTCTATTCTGTGCGAGCGGCGAGCAAGCAAGTGCAGAGCTGACTCCGCGGGAGCTGG 1839
QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 1840 CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGAGAGCTGCCAAATGGAATTTGGA 1899
QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuLysValGlySerGlnSer 505
Db 1900 CAGAGCATCATGTGCAGAGAACAGGTTCACGGGAAGAGCTGGGGAAAGTGGGAGTCTCAGTCT 1959

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QY 506 SerPheSerGlySerMetGluLeuIleGluValSer 517  
DB 1960 AGCTTTTCGGGAGGATGGAATCATTTGAGGTCTCC 1995

## RESULT 4

US-10-377-072-27  
; Sequence 27, Application US/10377072  
; Publication No. US20040157221A9  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Glucksman, Maria A.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Williamson, Mark J.  
; APPLICANT: Rudolph-Owen, Laura A.  
; APPLICANT: Chun, Miyoung  
; APPLICANT: Tsai, Fong-Ying  
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,  
; 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES  
; TITLE OF INVENTION: AND USES THEREFOR  
; FILE REFERENCE: MPI03-0180NMIM  
; CURRENT APPLICATION NUMBER: US/10/377,072  
; CURRENT FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: US 09/895,860  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215,370  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/723,806  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/187,455  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: US 09/843,297  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: US 60/199,801  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 09/861,801  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 60/205,508  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/816,494  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: US 09/815,419  
; PRIOR FILING DATE: 2001-03-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 1998  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)....(1998)  
US-10-377-072-27

Alignment Scores:  
Pred. No.: 4,43e-251 Length: 1998  
Score: 2606.00 Matches: 516  
Percent Similarity: 90.21% Conservative: 0  
Best Local Similarity: 90.21% Mismatches: 1  
Query Match: 97.68% Indels: 56  
DB: 19 Gaps: 1

US-09-964-277-21 (1-517) x US-10-377-072-27 (1-1998)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20  
DB 281 ATGTTGCCCTCTCTCTTCAGACTGTTTCTCACTGTAATCTCGGGTAAACTGGAGAAGA 340  
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29  
DB 341 GCTTCAACTCTGTTCACTGCTTGA-GGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCT 399

QY 29 ----- 29  
DB 400 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCAATTTCTACGCTTGTCTTACCT 459  
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DB 460 GTTCCCAACATTGGGCGCAACCCGAATTTCTCCCAATCTTTATCTTGGTGGCCGCGAGAT 519  
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45  
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QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65  
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QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGlnLeuSerGlu 305  
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QY 306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325  
DB 1360 CAGACTCCGAAACCAGTCTCTGATAAGGAGGAAGCAGCATCCCCAAGAAAGCTGCAGAC 1419  
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QY 346 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
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Db 1720 GGAGCAGTGCAGTTACTCTGCTTACAGCTGCAGCAGCTGCCACTTGGCGGAGACCA 1779
QY 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgSerTrp 465
Db 1780 GTCTATTCTGTGCGCAGCGCGCAGAACCAAGTGACAGAGCTGACTCGCGCGGAGCTGG 1839
QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 1840 CATGAAGAGAGCCCTTTTGAAGAAGAGTTTAAACGCAGAAAGCTGCCAAATGGAAATTGGA 1899
QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db 1900 GAGACATCATGCTCAGAGAACAGGTTCACGGNAGAGCTGGGGAAAGTGGGAGTCAGTCT 1959
QY 506 SerPheSerGlySerMetGluIleLeuGluValSer 517
Db 1960 AGCTTTTTCGGGCAGCATGGAAATCATTTGAGGTCTCC 1995
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## RESULT 5

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US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 673
; LENGTH: 2102
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-094-749-673
Alignment Scores:
Pred. No.: 4,77e-251 Length: 2102
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 17 Gaps: 1

US-09-964-277-21 (1-517) x US-10-094-749-673 (1-2102)
QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTyrValAsnTyrArgArg 20
Db 336 ATGTTGGCTCTCTCTCTTCAGACTGTTTTTCTCACTGACTCTTCTGGGTAACTGGAGAGA 395
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 396 GCTTCAACTCTGTTCACTGCTTGCA-GGTGGGTTTCTGTGAGTTCTCTCGTTGTTTCCCT 454
QY 29 ----- 29
Db 455 GGCCTCTGTGAAGAAATCCACTTAGTCCCTACCTGTCATTTCTCAGCCTTGCTTACCT 514
QY 29 ----- 29
Db 515 GTTCCCAACATTGGGCCAACCCCTAATTCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 574
QY 30 -----GluLeuMetGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 575 GTCTCTCAACAGGAGCTGATGCAGCAGATGGGATTGGTTATGTGTTAAATGCCAGCAAT 634
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db 635 ACCTGTCAAAAGCCTGACTTTATCCCGAGTCTCATTTCTCCGCTGTGCCTGTGAATGAC 694
QY 66 SerPheCysGluLysIleLeuProTyrLeuAspLysSerValAspPheIleGluLysAla 85
Db 695 AGCTTTTGTGAGAAATTTTGGCCGTGGTTGGACAAATCAGTAGATTTTCATTGAGANAGCA 754
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 755 AAAGCCTCCAATGGATGTTCTAGTGCACCTGTTTAGTGGGATCTCCCGCTCCGCCACC 814
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 815 ATCGCTATCGCTACATCATGAAGAGGATGACATGTCTTTAGATGAAGCTTACAGATTT 874
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 875 GTGAAGAAAAAAGACCTTACTATATCTCCAACCTTCAATTTTCTGGGCCAACTCTCTGGAC 934
QY 146 TyrGluLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db 935 TATGAGAAGAAGATTAAAGAACCCAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 994
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyLysSer 185
Db 995 CTGCACCTGGAGAAGCCAAATGAACCTGTCTCCTGTCTCAGAGGGTGGACAGAAAAAGC 1054
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1055 GAGACGCCCTTCAGTCCACCTGTGCCACTCTGCTACTCTCAGAGGACAGGACAAAGG 1114
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1115 CCGGTGCATCCGCCAGCGTCCCGAGCGTCCCGAGCGTGCAGCGCTGCTGTTAGAGGAC 1174
QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1175 AGCCCGCTGGTACAGGCGCTCAGTGGGCTGACCTGTCCGAGACAGCTGGAACAGAC 1234
QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
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Db 1235 AATAAGCTCAAGCGTTCCTCTCTGGATATCAAAATCAGTTTCATATTACGCCAGCATG 1294
Qy 266 AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrIysProSer 285
Db 1295 GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAAATACACAACTTCC 1354
Qy 286 ThrThrLeuAspGlyThrAsnIysLeuCysGlnPheSerProValGlnGlnLeuSerGlu 305
Db 1355 ACTACTCTGGATGGGACCAACAGCTATGCCAGTTCTCCCTGTTTCAGGAATATCGGAG 1414
Qy 306 GlnThrProGluThrSerProAspIysGluGluAlaSerIleProIysIysLeuGlnThr 325
Db 1415 CAGACTCCCGAAACCAAGTCTCTGATAAGGAGGAAGCCAGCATCCCAAGAAGTGCAGACT 1474
Qy 326 AlaArgProSerAspSerGlnSerIysArgLeuHisSerValArgThrSerSerGly 345
Db 1475 GCCAGCCTTCAGACGCCAGAGCAAGCATTCGATTCGGTCAGAACCCAGCAGTGGC 1534
Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db 1535 ACCGCCAGAGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1594
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrIysSerAlaGly 385
Db 1595 CACACCAGCTTCTTTTCGGCCTTTCCACAGCCAGCAGCCTCACGAAGTCTGCTGCG 1654
Qy 386 LeuGlyLeuIysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 1655 CTGGGCGCTTAAGGGCTGGGCACCTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCC 1714
Qy 406 ThrSerSerTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 1715 ACCAGCAGTGGTATTTTGGCCACAGAGTCTCACACTTCTACTCTGCCTCAGCCATCTAC 1774
Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 1775 GGAGGCAGTGCCAGTTACTCTGCTACAGCTGCAGCCAGCTGCCACCTTGGCGAGACCAA 1834
Qy 446 ValTyrSerValArgArgGlnIysProSerAspArgAlaAspSerArgSerTyr 465
Db 1835 GTCTATTCTGTGCGAGCGGCGAGAACCAAGTGCAGAGCTGACTCGCGCGGAGCTGG 1894
Qy 466 HisGluGluSerProPheGluIysGlnPheIysArgSerCysGlnMetGluPheGly 485
Db 1895 CATGAAGACAGGCCCTTTGAAAAGCATTTTAAACGACAGCTGCCAATGGAAATTGGA 1954
Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyIysValGlySerGlnSer 505
Db 1955 GAGAGCATCATGTTCAGAGAACAGGTTCACGGGAAGAGCTGGGAAAGTGGGCAAGTCACT 2014
Qy 506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db 2015 AGCTTTTCGGCAGCATGGAAATCATTTAGGTCTCC 2050
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RESULT 6

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US-10-168-506-2
; Sequence 2, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168, 506
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
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; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-168-506-2

Alignment Scores:
Pred. No.: 7e-251 Length: 2732
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 18 Gaps: 1

US-09-964-277-21 (1-517) x US-10-168-506-2 (1-2732)

Qy 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTyrValAsnTyrArgArg 20
Db 818 ATGTTGCCCTCTCTCTTTCAGACTGTTTTCCTCAGTGTACTTCTGGGTAACCTGGAGAAGA 877
Qy 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 878 GCTTCACCTCTGTTCACTGCTTGCA-CGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCT 936
Qy 29 ----- 29
Db 937 GGCCTCTGTGAAGGAATAATCCACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACCT 996
Qy 29 ----- 29
Db 997 GTTGCCAAATTTGGGCCCAACCCGAATCTTCCCAATCTTTATCTTTGGTGCAGCGAGAT 1056
Qy 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 1057 GTCTCTCAACAGGAGCTGATGACGACGAATGGGATGGTATGTTATGTTTAAATGCCAGCAAT 1116
Qy 46 ThrCysProIysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db 1117 ACCTGTCCAAAGCCTGACTTTATATCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGAC 1176
Qy 66 SerPheCysGluIysIleLeuProThrLeuAspIysSerValAspPheIleGluIysAla 85
Db 1177 AGCTTTTGTGAAAAATTTTGGCGGTGGGCAAAATCAGTAGATTTTCATTGAGAAAGCA 1236
Qy 86 IysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 1237 AAAGCCTTCAATGGATGTGTTCTAGTGCACTGTTTAGTGGGATCTCCGCTCCGCCACC 1296
Qy 106 IleAlaIleAlaTyrIleMetIysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 1297 ATCGTATCGCTACATCATGAAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATTT 1356
Qy 126 ValIysGluIysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 1357 GTGAAAGAAAAAGACCTACTATATCTCCAAATTTCTGGGCCCACTCTCTGGAC 1416
Qy 146 TyrGluIysIysIleIysAsnGlnThrGlyAlaSerGlyProIysSerIysLeuIysLeu 165
Db 1417 TATGAGAAGAGATTAAAGAACCACTGAGACTGAGGATCAGGGCCCAAGAGCAAACTCAAGCTG 1476
Qy 166 LeuHisLeuGluIysProAsnGluProValProAlaValSerGluGlyGlnIysSer 185
Db 1477 CTGCACCTTGGAGAGCCAAATGAACCTGTCTCTGCTGTCTCAGAGGGTGGACAGAAAAAGC 1536
Qy 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArg 205
Db 1537 GAGACGCCCTCAGTCCACCTGTGCCACTCTGTCTACTCTCAGAGGCGACAGCAAAAGG 1596
Qy 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1597 CCCGTGTCATCCCGCCAGCGTGCCTCCAGCGTGCCTGCTGCTGTTAGAGGAC 1656
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Qy	226	SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer	245
Db	1657	AGCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGACAGCAGGCTGGAAGACAGC	1716
Qy	246	AsnLysLeuLysArgSerPheSerLeuAspLleLysSerValSerTyrSerAlaSerMet	265
Db	1717	AATAAGCTCAAGCGTCTCTCTCTCGATATCAAAATCAGTTTCATATTCAGCCGACGATG	1776
Qy	266	AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer	285
Db	1777	GCAGCATCCTTACATGCGTCTCTCTCATCAGAGATGCTTTGGAACTACTACAAACCTTCC	1836
Qy	286	ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu	305
Db	1837	ACTACTCTGGATGGACCAACAAGCATATGCCAGTTCTCCCTGTCTCAGGAACATATCGGAG	1896
Qy	306	GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr	325
Db	1897	CAGATCCCCAAACAGTCTCTGATAAGAGAGAGCCAGCATCCCAAGAAGCTGCAGACT	1956
Qy	326	AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly	345
Db	1957	GCCAGGCTTCAGACAGCCAGAGCAAGGATTGCATTCCGTCAGAACCCAGCAGCAGTGGC	2016
Qy	346	ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr	365
Db	2017	ACCGCCACAGAGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGGTGGAGGACAAATTAC	2076
Qy	366	HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly	385
Db	2077	CACACCAGCTTCCTTTTCGGCCTTTCACACAGCCAGCAGCACCTTCACGAAGTCTGCTGGC	2136
Qy	386	LeuGlyLeuLysGlyTyrHisSerAspLleLeuAlaProGlnThrSerThrProSerLeu	405
Db	2137	CTGGGCCTTAAGGCTGGCACTCGGATATCTTTGGCCCCCAGACCTCTACCCCTTCCCTG	2196
Qy	406	ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr	425
Db	2197	ACCAGCAGCTGGTATTTGGCACAGAGTCTTCACACTTCTACTCTGCTCTCAGCCATCTAC	2256
Qy	426	GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln	445
Db	2257	GGAGCAGTGCAGTTACTCTGCCTCAGCTGACCCAGCTGCCCATCTTGGGAGACCAA	2316
Qy	446	ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp	465
Db	2317	GTCTATTCTGTGCGCAGCGCGCAGAACCAAGTCACAGAGCTGACTCGCGCGGAGGTGG	2376
Qy	466	HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly	485
Db	2377	CATGAAGAGAGACCCCTTTTGAAGAAGCAGTTTAAACGCAGAGACTGCCAAATGGAAATTGG	2436
Qy	486	GluSerIleMetSerGluAsnArgSerArgGluLeuGluLysValGlySerGlnSer	505
Db	2437	CAGAGCATCATGTCAGAGAACAGGTACCGGAGAGGCTGGGGAAAGTGGGCGAGTCAGTCT	2496
Qy	506	SerPheSerGlySerMetGluIleGluValSer	517
Db	2497	AGCTTTTCGGGCAGCATGGAATCATTTAGGCTCTCC	2532

## RESULT 7

126	VallYsGluLysAtrgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp	145
1357	GTGAAGAAGAAAAGACCTACTATATCTCAAACTTCAATTTCTGGGCCAACTCTGGAC	1416
146	TyrGluLysLysIleLysAsnGlnThrGlyIleSerGlyProLysSerLysLeuLeuLeu	165
1417	TATGAGAAGAAGATTAAACACAGACTGAGCATCAGGGCCAAAGACCAACTCAAGCTG	1476
166	LeuHisLeuGluLysProAsnGluProValProIaValSerGluGlyGlyGlnLysSer	185
1477	CTGCACCTGGAGAACCCAAATGAACCTGCTCCCTCGCTCTCAGAGGGTGGACAGAAAGC	1536

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186  GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaGlyGlnArg 205
1537  GAGAGCCCTCAGTCCACCTGTGCCGACTCTGTACTCTCAGAGCAGCAGCAAGG 1596
206  ProValHisProAlaSerValProSerValProSerValGlnProSerLeuGluAsp 225
1597  CCGGTGATCCCGCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGT 1656
226  SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuAspSer 245
1657  AGCCCGCTGTACAGCGCTCAGTGGCTGCACCTGTCCGACAGCAGGCTGGAACAGC 1716
246  AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
1717  AATAGCTCAGGGTTCCTCTCTCTGGATATCAATCAGTTTCATATTCACCGCATG 1776
266  AlaAlaSerLeuHisGlyPheSerSerGluAlaSerIleProLysLysLeuGlnThr 285
1777  GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAATACTACAAACCTCC 1836
286  ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnLysSerGlu 305
1837  ACTACTCTGGATGGGACCAAGCTATCCGACTTCTCCCTGTTCAGGAATATCGGAG 1896
306  GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325
1897  CAGACTCCCGAAACCACTCTGATAGAGGAGGAGCCAGCATCCCAAGAGCTGCAGCT 1956
326  AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345
1957  GCCAGGCTTCAGACAGCCAGCAGCAGCATTCGATTCGCTCAGAACAGCAGCAGTGC 2016
346  ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
2017  ACCGCCAGAGGTCCCTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGCAATAC 2076
366  HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
2077  CACACAGCTTCTTTTCGGCTTTCCACAGCCAGCAGCAGCATTCAGAGTCTGCTGC 2136
386  LeuGlyLeuLysGlyTyrHisAspIleLeuAlaProGlnThrSerThrProSerLeu 405
2137  CTGGGCTTAAGGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2196
406  ThrSerSerTyrTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
2197  ACCAGCAGCTGTGTATTTTGGCAGAGTCTCAGACTTCTACTCTGCCTCAGCCATCTAC 2256
426  GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
2257  GGAGGAGTCCAGTGTACTCTGCTCAGCTGAGCTGAGCAGCTGCTGCTGCTGCTGCTG 2316
446  ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTyr 465
2317  GTCTATTCTGTGCGAGCGGCGAGAGCCAGTGCAGAGCTGACTCGCGCGGAGCTG 2376
466  HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
2377  CATGAAGAGAGCCCTTTGAAAAGCAGTGTAAACGCGAAGCTGCCAAATGGAAATTTGA 2436
486  GluSerIleMetSerGluAsnArgSerArgGluLeuGlyValGlySerGlnSer 505
2437  GAGAGCATCATGTACAGAAACAGGTACCGGAGAGAGCTGGGGAAGTGGGCGAGTCTCT 2496
506  SerPheSerGlySerMetGluIleIleGluValSer 517
2497  AGCTTTTCGGCGCAGCATGGAAATCATTTAGGTCTCC 2532

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RESULT 8

US-10-296-115-520

; Sequence 520, Application US/10296115

; Publication No. US20040053248A1

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; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 520
; LENGTH: 2966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2966)
; OTHER INFORMATION: n = a,t,c or g
US-10-296-115-520

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Alignment Scores:
Pred. No.: 7,89e-251 Length: 2966
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 18 Gaps: 1

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US-09-964-277-21 (1-517) x US-10-296-115-520 (1-2966)

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QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheThrValAsnTrpArgArg 20
DB 303 ATGTGCTCTCTCTCTCTTTCAGACTGTTTCTCAGTACTTCTGCGTAAACTGGAGAAGA 362
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
DB 363 GCTTCAACTCTGTTTCACTGCTTGCA-GGTGGGTTTGTGTGAGTTCTCTCGTTGTTTCCCT 421
QY 29 ----- 29
DB 422 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 481
QY 29 ----- 29
DB 482 GTTGCCAACTATGGGCCAACCGAATCTTCCCAATCTTTATCTTGTGGCTGCCAGCAGAT 541
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
DB 542 GTCTCTCAACAGGAGCTGATGCAGCAGAAATGGGATTTGTTATGTGTTAAATGCCAGCAAT 601
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
DB 602 ACCTGTCAAAGCCGTGACTTTATCCCGAGTCTCATTTCTCGGTGCTGCTGTGAATGAC 661
QY 66 SerPheCysGluLysIleLeuProThrLeuAspLysSerValAspPheIleGluLysAla 85
DB 662 AGCTTTGTGAGAAATTTTGGCGTTGGCAAAATCAGTAGATTTTCATTGAGAAGCA 721
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
DB 722 AAAGCCTCCAATGGATGTGTTCTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 781
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
DB 782 ATCGCTATCGCTACATCATATGAAGAGGATGGACATGCTCTTTAGTAGAAGCTTACAGATT 841
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
DB 842 GTGAAGAGAAAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGAC 901
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165

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Db 902 TATGAGAGAGATTAAAGACAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 961  
Qy 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185  
Db 962 CTGACCTGGAGAGCAAAAGTAACTGCTCCCTGCTGTCTCAGAGGGTGGACAGAAAAAGC 1021  
Qy 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205  
Db 1022 GAGAGCCCTCAGTCCACCTGTGCCACTCTGTACTCAGAGGCAGCAGGACAAAGG 1081  
Qy 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225  
Db 1082 CCCGTGCATCCGCCAGCGTCCAGAGGTGCCAGCGTGCAGCGCTCGCTGTAGAGGAC 1141  
Qy 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245  
Db 1142 AGCCCGCTGGTACAGCGCTCAGTGGGTGCACCTGTCCGACAGCAGGCTGGAAGACAGC 1201  
Qy 246 AsnLysLeuLysArgSerPheSerLeuAspLleLysSerValSerTyrSerAlaSerMet 265  
Db 1202 AATAAGCTCAAGCGTTCTCTCTGGATATCAATCAGTTTCATATTCAGCCAGCATG 1261  
Qy 266 AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer 285  
Db 1262 GCAGCATCTTACATGGCTTCTCTCATCAGAGATGCTTTGGATATCTACAACTTCC 1321  
Qy 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnLeuSerGlu 305  
Db 1322 ACTACTCTGGATGGGACCAACAGCTATGCTCAGATTCTCCCTGTTCAGGAACATATCGGAG 1381  
Qy 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325  
Db 1382 CAGACTCCGAAACACAGTCTCTATAGGAGGAAGCCAGCATCCCAAGAGCTGCAGACC 1441  
Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345  
Db 1442 GCCAGCCTTCAGACGCCAGCAGCAGCGATTGGATTGGTCAGAACCCAGCAGCTGGC 1501  
Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365  
Db 1502 ACCGCCACAGGTTCCTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 1561  
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385  
Db 1562 CACACCAGCTTCTTTTCGGCTTTTCCACAGCCAGCAGCACCCTCACGAAGTCTGCTGGC 1621  
Qy 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405  
Db 1622 CTGGGCTTTAAGGCTGGCAGCTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 1681  
Qy 406 ThrSerSerTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425  
Db 1682 ACCAGCAGCTGGTATTTTCCACAGAGTCTCTCACACTTCTACTCTGCCTCAGCCATCTAC 1741  
Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445  
Db 1742 GGAGGCAGTGCCAGTTACTCTGCCTACAGCTCAGCCAGCTGCCACTTGGCGGAGCCAA 1801  
Qy 446 ValTyrSerValArgArgGlnLysProSerAspAtqAlaAspSerArgArgSerTrp 465  
Db 1802 GTCATTTCTGTGGCAGGCGGAGAGCCAGGAGTGAACAGCTGATCTCGCGCGGAGCTGG 1861  
Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485  
Db 1862 CATGAAGAGAGCCCCCTTTGAAAGACGATTTAAACGCAGAGCTGCCAAATGGAATTTGA 1921  
Qy 486 GluSerIleMetSerGlnAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505  
Db 1922 GAGAGCATATGTCAGAGAACAGGTACGGGAAGAGCTGGGAAAGTGGGCAGTCAGTCT 1981  
Qy 506 SerPheSerGlySerMetGluIleLeuGluValSer 517  
Db 1982 AGCTTTTCGGGAGCATGGAATCATTGAGGCTCC 2017

## RESULT 9

US-10-257-026-1  
; Sequence 1, Application US/10257026  
; Publication No. US20040086859A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; TITLE OF INVENTION: New dual specificity phosphatase  
; FILE REFERENCE: DUSP10KWS  
; CURRENT APPLICATION NUMBER: US/10/257,026  
; CURRENT FILING DATE: 2003-11-07  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3059  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (127)..(2121)  
US-10-257-026-1

## Alignment Scores:

Pred. No.: 8,26e-251 Length: 3059  
Matches: 516  
Score: 2606.00 Conservative: 0  
Percent Similarity: 90.21%  
Best Local Similarity: 90.21%  
Query Match: 97.68%  
Indels: 56  
Gaps: 1

US-09-964-277-21 (1-517) x US-10-257-026-1 (1-3059)

Qy 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20  
Db 407 ATGTTGGCTCTCTCTCTCAGACTGTTTCTCAGCTACTTCTGGTAACTGGAGAAAGA 466  
Qy 21 AlaSerThrLeuPheThrCysLeuGln----- 29  
Db 467 GCTTCAACTCTGTTTCACTGCTTGCA-GGTGGGTTTGTGTGAGTCTCTCGTTGTTTCCCT 525  
Qy 29 ----- 29  
Db 526 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACCT 585  
Qy 29 ----- 29  
Db 586 GTTGCAACATTGGGCCAACCCGAATCTTCCCAATCTTTATCTTTGGCTGCCAGCGAGAT 645  
Qy 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45  
Db 646 GTCCTCAACAAGGAGCTGATCAGCAGAAATGGGATTTGTTATGTGTTAAATGCCAGCAAT 705  
Qy 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65  
Db 706 ACCTGTCCAAAGCCTGACTTTATCCCCAGCTCATTTCTCGGCTGCTGTGAATGAC 765  
Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85  
Db 766 AGCTTTTGTGAGAAAAATTTTCCCGTGGTTGGACAAATCAGTAGATTTTCATTGAGAAAGCA 825  
Qy 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105  
Db 826 AAAGCCTCAATGATGTTCTAGTGACCTGTTTAGCTGGGATCTCCGCTCCGCCACC 885  
Qy 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125  
Db 886 ATCGCTATCGCTACATCATGAGAGGATGGACATGTTCTTTAGATGAAGTTACAGATTT 945  
Qy 126 VallysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145  
Db 946 GTGAAAGAAAAAAGACCTTACTATATCTCCAAACTTCAATTTTCTGGGCAACTCTCTGGAC 1005  
Qy 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLeu 165

Db 1006 TATGAGAGAGATTAAAGAACAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 1065  
QY 166 LeuHisLeuGluYsProAsnGluProValProAlaValSerGluGlyGlnYsSer 185  
Db 1066 CTCGACCTGGAGAAGCAATGAACCTGTCCCTGTCTCAGAGGGTGGAGAGAAAGC 1125  
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205  
Db 1126 GAGAGCCCTCAGTCCACCTGTGCCGACTCTGTACTCTCAGAGGCAGCAGACAAAGG 1185  
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225  
Db 1186 CCGTGCATCCCGCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCTGTGTAGAGGAC 1245  
QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245  
Db 1246 AGCCCGCTGGTACAGCGCTCAGTGGGTGCCACCTGTCCGACAGAGCGTGGAAACAGC 1305  
QY 246 AsnLysLeuLysArgSerPheSerLeuAspLysSerValSerValSerAlaSerMet 265  
Db 1306 AATAAGCTCAGGGTTCCTTCTCTCTGGATATCAATCAGTTCATATTCAGCCAGCATG 1365  
QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAlaLeuGluTyrTyrLysProSer 285  
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QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnLeuLeuSerGlu 305  
Db 1426 ACTACTCTGGATGGGACCAACAGCTATGCCAGTTCCTCCCTGTTCAGGAACATATCGGAG 1485  
QY 306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325  
Db 1486 CAGACTCCCGAAACCAAGTCTGTATAGAGAGAGAGCCAGCATCCCAAGAGTGTGAGACC 1545  
QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345  
Db 1546 GCCAGCCCTTCAGACAGCCAGCAGCAGCATTCGATTCGTCAGAACACAGCAGCATTCAC 1605  
QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365  
Db 1606 ACCGCCAGAGGTCCCTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAAATTAC 1665  
QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385  
Db 1666 CACACAGCTTCTTTTTCGGCCCTTCACACAGCAGCAGCAGCATCTCAGAAAGTCTGCTGC 1725  
QY 386 LeuGlyLeuLysGlyThrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405  
Db 1726 CTGGGCTTAAAGGCTGGGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTG 1785  
QY 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425  
Db 1786 ACCAGCAGCTGGTATTTTGGCCAGAGTCTCACACTTCTACTCTGCCTCAGCCATCTAC 1845  
QY 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445  
Db 1846 GGAGGAGTGGTCCAGTACTCTGCCTACAGCTGAGCCAGCGTGGCCACTTTCGGGAGACCAA 1905  
QY 446 ValTyrSerValArgArgGlnLysProSerAspAlaAspSerArgArgSerTrp 465  
Db 1906 GTCTATTCTGTGGCAGCGCGAGAGCCAGCCAAAGTGTACAGACTGACTCGCGCGGAGCTGG 1965  
QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485  
Db 1966 CATGAGAGAGCCCTTTTGAAGAGCAGTTTAAACGCGAGAGCTGCCAAATGGAAATTGGA 2025  
QY 486 GluSerIleMetSerGluAnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505  
Db 2026 GAGAGCATCATGTCCAGAGAACAGTCCAGGGAGAGCTGGGGAAAGTGGGCGAGTCACTGCT 2085  
QY 506 SerPheSerGlySerMetGluIleLeuGluValSer 517

Db 2086 AGCTTTTGGGCAGCATGGAAATCATTTAGAGTCTCC 2121  
RESULT 10  
US-09-964-277-1  
; Sequence 1, Application US/09964277  
; Patent No. US20020317170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125,434  
; CURRENT APPLICATION NUMBER: US/09/964,277  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3496  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-277-1  
Alignment Scores:  
Pred. No.: 1e-250 Length: 3496  
Score: 2606.00 Matches: 516  
Percent Similarity: 90.21% Conservative: 0  
Best Local Similarity: 90.21% Mismatches: 1  
Query Match: 97.68% Indels: 56  
Gaps: 1  
DB: 1  
US-09-964-277-21 (1-517) x US-09-964-277-1 (1-3496)  
QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20  
Db 842 ATGTTCCTCTCTCTCTCTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAGA 901  
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29  
Db 902 GCTTCAACTCTGTTCCACCTGCTTGCA-GGTGGTGTGTGTGAGTTCCTCGTGTGTTCCCT 960  
QY 29 ----- 29  
Db 961 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1020  
QY 29 ----- 29  
Db 1021 GTTGCCAACTTTGGSCCAACCGAATCTTCCCAATCTTTATCTTGGCTGCCAGCGAGAT 1080  
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45  
Db 1081 GTTCCTCAACAGGAGCTGATGCAGCAGAAATGGGATTTGTTATGTGTTAAATGCCAGCAAT 1140  
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65  
Db 1141 ACCTGTCCAAAGCCGTGACTTTATCCCGAGTCTCAATTTCTCGCTGTGCTGTGATGAC 1200  
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85  
Db 1201 AGCTTTTGTGAGAAATTTTGGCGTGTGGACAAATCAGTAGATTTTCATTGAGAAAGCA 1260  
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105  
Db 1261 AAAGCCTCCAAATGGATGTGTTCTAGTGCACTCTTTAGTGGGATCTCCCGCTCCGCCACC 1320  
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125  
Db 1321 ATCGCTATCGCTACATCATGAGAGGATGGACATGTCTTTAGATGAAGCTTACAGATT 1380  
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145  
Db 1381 GTGAAGAGAAAGAAAGCTTACTATATCTCCAACTTCAATTTCTGGGCCAATCTCTGGAC 1440  
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165



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Db 1441 TATGAGAAGAGATTAAAGACAGACTGGAGCATCAGGCCCAAGAGCAAACTCAAGCTG 1500
Qy LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
Db 1501 CTGACCTGGAGAAGCAAAATGAACCTGTCCCTGTGTCTCAGAGGGTGGACAGAAAAGC 1560
Qy 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1561 GAGAGCCCCCTCAGTCCACCCCTGTCCGACTCTGTACTCTCAGAGGCAGCAGCAAAAGG 1620
Qy 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1621 CCCGTGCATCCCGCAGCGTGCCAGCGTGCCAGCGTGCGAGCCGTGCTGTGTAGAGGAC 1680
Qy 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1681 AGCCCGCTGGTACAGCGCTCAGTGGGTGCACCTGTCCGACAGACAGGCTGGAAGACAGC 1740
Qy 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db 1741 AATAAGCTCAAGCGTTCCCTCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGCATG 1800
Qy 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db 1801 GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAAATACACAACTTCC 1860
Qy 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db 1861 ACTACTCTGATGGGACCAACAAAGTATGCCAGTGTCTCCCTGTTTCAGGAACATATCGGAG 1920
Qy 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db 1921 CAGACTCCCGAAACCACTCTCATTAAGGAGGAAGCAGCATCCCAAGAAAGCTGCAGACC 1980
Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerGly 345
Db 1981 GCCAGCCCTTCAGACAGCCAGCAGCAGCGATTTGCATTCGGTCAGAACCCAGCAGAGTGC 2040
Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db 2041 ACCGCCACAGGTCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATTAC 2100
Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 2101 CACACCAGCTTCTCTTTCGGCCCTTTCCACCAGCCAGCAGCACCCTCACGAAGTCTGCTGC 2160
Qy 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 2161 CTGGGCTTTAAGGCTGGCAGCTCGGNATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2220
Qy 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 2221 ACCAGCAGCTGGTATTTTGGCCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 2280
Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 2281 GGAGGCGAGTGCAGGTACTCTGCCTACAGCTGCAGCCAGCTGCCACCTTGGCGGAGACCAA 2340
Qy 446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db 2341 GTCTATCTGTGGCGAGGCGGAGAGCCAAAGTGAAGAGTGCAGAGCTGCCTGGCGGAGAGTGG 2400
Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 2401 CATGAAGAGAGCCCCCTTTGAAAGGACAGTTTAAACGCAGAAAGCTGCCAAATGGAATTTGA 2460
Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
Db 2461 GAGAGCATCATGTTCAGAGAACAGGTACCGGGAAGAGCTGGGAAAAGTGGGCAGTCAGTCT 2520
Qy 506 SerPheSerGlySerMetGluIleIleGluValSer 517
Db 2521 AGCTTTTCCGGGACGATGGAAATCATTTGAGGTCTCC 2556
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## RESULT 11

US-10-370-715B-261  
; Sequence 261, Application US/10370715B  
; Publication No. US20040258678A1  
; GENERAL INFORMATION:

; Patin Docket Preview

; APPLICANT: BODARY, SARAH C.

; APPLICANT: CLARK, HILLARY

; APPLICANT: BRISDELL, HUNTE

; APPLICANT: JACKMAN, JANET

; APPLICANT: SCHOENFELD, JILL R.

; APPLICANT: WILLIAMS, P. MICKEY

; APPLICANT: WOOD, WILLIAM I.

; APPLICANT: WU, THOMAS D.

; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune

; FILE REFERENCE: P1949R1-US

; CURRENT APPLICATION NUMBER: US/10/370,715B

; CURRENT FILING DATE: 2003-02-21

; NUMBER OF SEQ ID NOS: 742

; SEQ ID NO 261

; LENGTH: 3521

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-370-715B-261

Alignment Scores:  
Pred. No.: 1,01e-250 Length: 3521  
Score: 2606.00 Matches: 516  
Percent Similarity: 90.21% Conservative: 0  
Best Local Similarity: 90.21% Mismatches: 1  
Query Match: 97.68% Indels: 56  
DB: 20 Gaps: 1

US-09-964-277-21 (1-517) x US-10-370-715B-261 (1-3521)

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Qy 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db 844 ATGTTGGCTCTCTCTCTCTCAGACTGTTTCTCTCACTACTTCTGGGTAACCTGGAGAAGA 903
Qy 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 904 GCTTCAACTGTTTCACTGCTGCTGCA-GGTGGGTTTGTGTGAGTCTCTCGTTGTTCCCT 962
Qy 29 ----- 29
Db 963 GGCCTCTGTGAAGGAAATCCACTCTAGTCCCTACTGCAATTTCTCAGCCTTGTCTTACCT 1022
Qy 29 ----- 29
Db 1023 GTTGCCAACATTGGGCCAACCGAATTTCTCCCAATCTTTATCTTTGGCTGCCAGCAGAT 1082
Qy 30 -----GluLeuMetGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 1083 GTCCTCAACAAGGAGCTGATCAGCAGAAATGGGATTTGTTATGTATGTTAAATGCCAGCAAT 1142
Qy 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db 1143 ACCTGTCCAAAGCCCTGACTTTATCCCGAGTCTCATTTCTCGGTGCTGCTGTGAATGAC 1202
Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db 1203 AGCTTTTGTGAGAAAATTTTCCGCTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAAGCA 1262
Qy 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 1263 AAAGCCTCCAAATGGAATGTTTCTAGTGACCTGTTTAGCTGGGATCTCCGCTCCGCCACC 1322
Qy 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 1323 ATCGCTATCGCTACATCATGAAGAGGATGCACATGTCTTTAGATGAAGCTTACAGATTT 1382
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QY 126 VallysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 1383 GTGAAGAAAAGACCTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGAC 1442
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db 1443 TATGAGAAGAGATTAAAGAACAGACTGGAGCATCAGGCGCCAAAGAGCAAACTCAAGCTG 1502
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlnLysSer 185
Db 1503 CTCGACCTGGAGAGCCAAATGAACCTGTCCTCTGCTCAGAGGTGGAGCAGAAAGC 1562
QY 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1563 GAGAGCCCTCAGTCCACCTGTGCCGACTCTGCTACCTCAGAGCGCAGCAGCAAAAGG 1622
QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1623 CCGGTGCATCCGCGCAGCGTCCGAGCGTCCGAGCGTGCAGCCGTCGCTGTTAGAGGAC 1682
QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1683 AGCCCGCTGGTACAGCGCTCAGTGGCTGCACCTGTCCGACAGACGGCTGGAGACAGC 1742
QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db 1743 NATAGCTCAGGGTCTCTCTCTGGATATCAATCAGTTTCAATATTCAGCCAGCATG 1802
QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db 1803 GCAGCATCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAATPACTACAAACCTTCC 1862
QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db 1863 ACTACTCTGGATGGGACCAACAGCTATGCCAGTCTCTCCCTGTTCCAGGAATATCGGAG 1922
QY 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db 1923 CAGACTCCCGAAACCAAGTCTCTGNTAAGGAGGAGCCAGCATCCCCAAGAGCTGCAGACC 1982
QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db 1983 GCCAGGCCCTCAGACAGCCAGAGCAAGCATTCGATTCGATCAGAAACAGCAGCAGTGCC 2042
QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspSerTyr 365
Db 2043 ACCGCCCAGAGGTCCCTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGCAATATAC 2102
QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 2103 CACACAGCTTCTCTTTTGGCCCTTCCACAGCCAGCAGCAGCATCAGAGTCTGCTGGC 2162
QY 386 LeuGlyLeuLysGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 2163 CTGGGCTTAAGGCTGGCAGCTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTG 2222
QY 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 2223 ACCAGCAGCTGGTGTATTTTGGCACAGATCTCTACACTTCTACTCTCGCTCAGCACTTAC 2282
QY 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 2283 GGAGGCAAGTGCCTACTCTGCTTACAGCTGAGCCAGCTGACCTCGCGCGGAGCCAA 2342
QY 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db 2343 GTCTATTCTGTGCGAGCGCGCAGAGCCAAAGTGACAGAGCTGACTCGCGCGGAGCTGG 2402
QY 466 HisGluGlnSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
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QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505
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Db 2463 GAGAGCATCATGTCTCAGAGAACAGGTCAAGGAAAGAGCTGGGAAAAGTGGCGAGTCAGTCT 2522
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Db 2523 AGCTTTTCGGGACGACATGGAAATCATTTGAGGTCTCC 2558

RESULT 12
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 1,02e-250 Length: 3544
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 9 Gaps: 1

US-09-964-277-21 (1-517) x US-09-816-494-1 (1-3544)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db 869 ATGTGGCCCTCTCTCTCTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAGAAAG 928
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 929 GCTTCAACTCTGTTCACTCTTGCA-GGTGGGTTTGTGAGTTCTCTCGTTGTTCCCT 987
QY 29 ----- 29
Db 988 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACCT 1047
QY 29 ----- 29
Db 1048 GTTGCCAAATTTGGGCCAACCCGAAATCTTCCAAATCTTTATCTTGGTCCGAGGAGAT 1107
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 1108 GTTCCTCAACAGAGAGCTGATGCAGAGAAATGGGATTTGTTATGTTTAAATGCCAGCAAT 1167
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAep 65
Db 1168 ACTGTCCAAAGCCTGACTTTATCCCGAGTCTCTATTTCTCGGTGCTGCTGTAATGAC 1227
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db 1228 AGCTTTTGTGAGAAAATTTTGGCGGTGGCAAAATCAGTAGATTTTCATTGAGAAAGCA 1287
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 1288 AAAGCCTCCAATGGATGTGTCTTAGTGCACTGTTTAGTGGGATCTCTCCGCTCCGCCACC 1347
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QY 106 IleAlaIleAlaTyrlleWetlylsArgMetSerLeuAspGluAlaTyrlArgPhe 125  
 Db 1348 ATCGCTATCGCTCATCATGAAGAGGATGGACATGCTTTAGATGAAGCTTACAGATT 1407  
 QY 126 VallylsGluLyArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145  
 Db 1408 GTGAAGAAAAAAGACCTTACTATATCTCCAACTTCAATTTCTGGGCCAACTCTCTGGAC 1467  
 QY 146 TyrGluLyLysIleLeuAsnGlnThrGlyAlaSerGlyProLyserLyserLyserLeu 165  
 Db 1468 TATGAGAAAGATTAAGAACACAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 1527  
 QY 166 LeuHisLeuGluLyProAsnGluProValProAlaValSerGluGlyGlyGlnLyser 185  
 Db 1528 CTGCACCTGGAGAACCAAACTGTCCCTGTCTCTCAGAGGGTGGACAGAAAAAGC 1587  
 QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205  
 Db 1598 GAGAGCCCTCAGTCCACCTGTGCCGACTCTGTACTCTCAGAGGCAGCAGCAAAAGG 1647  
 QY 206 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGluAsp 225  
 Db 1648 CCGCGTCATCCCGCCAGCGTCCAGCGTCCAGCGTCCAGCGTCCAGCGTCTGTAGAGGAC 1707  
 QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245  
 Db 1708 AGCCCGCTGGTACAGCGCTCAGTGGCGTGCACCTGTCCGACAGAGCGTGAAGACAGC 1767  
 QY 246 AsnLyLeuLyArgSerPheSerLeuAspIleLyserValSerValSerAlaSerMet 265  
 Db 1768 AATAAGCTCAAGGGTCTCTCTCTCTGGATATCAATCAGTTTCATATTCAGCCAGCATG 1827  
 QY 266 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluTyrlTyrlLyserProSer 285  
 Db 1828 GCAGCATCTTACATGGCTTCTCTCTCATCAGAAGATGCTTTGGAATACTACAAACCTTCC 1887  
 QY 286 ThrThrLeuAspGlyThrAsnLyserCysGlnPheSerProValGlnGluLeuSerGlu 305  
 Db 1888 ACTACTCTGGATGGGACCAACAAAGTATGCTCCAGTTCCTCCCTGTTTCAGGAACATATCGGAG 1947  
 QY 306 GlnThrProGluThrSerProAspLyserGluAlaSerIleProLyserLyserLeuGlnThr 325  
 Db 1948 CAGACTCCCGAAACCACTCTCTGATGAAGAGGAGGAGCAGCATCCCAAGAGCTGAGACC 2007  
 QY 326 AlaArgProSerAspSerGlnSerLyserArgLeuHisSerValArgThrSerSerGly 345  
 Db 2008 GCCAGGCTTCAGACAGCCAGAGCAAGCGATTGCAATTCGTTCAAGAACAGCAGCAGTGGC 2067  
 QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspSerTyr 365  
 Db 2068 ACCGCCACAGAGTCCCTTTATCTCCACTGCATCGAAGTGGAGCGTGGAGGACAAATTAC 2127  
 QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLyserSerAlaGly 385  
 Db 2128 CACACAGAGTCTCTTTTCGGCTTTCCACAGCCAGCAGCAGCTCACGAGTCTGCTGGC 2187  
 QY 386 LeuGlyLeuLyGlyTrpHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405  
 Db 2188 CTGGGCTTTAAGGGCTGGCACTCGGATATCTTTGGCCCCCAGACCTTACCCCTTCCCTG 2247  
 QY 406 ThrSerSerTrpTyrlPheAlaThrGluSerSerHisPheTyrlSerAlaSerAlaIleTyr 425  
 Db 2248 ACCAGCAGTGTGTATTTTCCACAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 2307  
 QY 426 GlyGlySerAlaSerTyrSerAlaTyrlSerCysSerGlnLeuProThrCysGlyAspGln 445  
 Db 2308 GGAGGAGTGGCCAGTTACTCTGCTTACAGCTCAGCCAGCTGCCACCTTGGAGGCCAA 2367  
 QY 446 ValTyrlSerValArgArgGlnLyserProSerAspArgAlaAspSerArgSerTrp 465  
 Db 2368 GTCTATTCTGTGCGGAGGCGGAGCAAGTGCAGAGCTCACTCGCGCGGAGCTGG 2427  
 QY 466 HisGluGluSerProPheGluLyserGlnPheLyserArgSerCysGlnMetGluPheGly 485

Db 2428 CATGAAGAGAGCCCTTTGAAAGACAGCTTTAAACGCAGAGCTGCCAAATGGAATTGGA 2487  
 QY 486 GluSerIleMetSerGluAsnArgSerArgGluGluIleuGlyLyserValGlySerGlnSer 505  
 Db 2488 GAGAGCATCATGTGCAGAGAACAGGTCACTGCGGAGAGAGCTGGGGAAGTGGGCGAGTCAGTCT 2547  
 QY 506 SerPheSerGlySerMetGluIleIleGluValSer 517  
 Db 2548 AGCTTTTCGGCAGCAGTGAATCATTTGAGGTCTCC 2583

RESULT 13

US-10-377-072-25  
 ; Sequence 25, Application US/10377072  
 ; Publication No. US20040009501A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals Inc.  
 ; APPLICANT: Curtis, Rory A.J.  
 ; APPLICANT: Logan, Thomas Joseph  
 ; APPLICANT: Glucksmann, Maria A.  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: Williamson, Mark J.  
 ; APPLICANT: Rudolph-Owen, Laura A.  
 ; APPLICANT: Chun, Miyoung  
 ; APPLICANT: Tsai, Fong-Ying  
 ; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,  
 ; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES  
 ; TITLE OF INVENTION: AND USES THEREFOR  
 ; FILE REFERENCE: MPI03-0180NMIM  
 ; CURRENT APPLICATION NUMBER: US/10/377,072  
 ; CURRENT FILING DATE: 2003-02-27  
 ; PRIOR APPLICATION NUMBER: US 09/895,860  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/215,370  
 ; PRIOR FILING DATE: 2000-06-29  
 ; PRIOR APPLICATION NUMBER: US 09/723,806  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: US 60/187,455  
 ; PRIOR FILING DATE: 2000-03-07  
 ; PRIOR APPLICATION NUMBER: US 09/843,297  
 ; PRIOR FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: US 60/199,801  
 ; PRIOR FILING DATE: 2000-04-26  
 ; PRIOR APPLICATION NUMBER: US 09/861,801  
 ; PRIOR FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: US 60/205,508  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 09/816,494  
 ; PRIOR FILING DATE: 2001-03-23  
 ; PRIOR APPLICATION NUMBER: US 09/815,419  
 ; PRIOR FILING DATE: 2001-03-22  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 25  
 ; LENGTH: 3544  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (589) ... (2586)  
 US-10-377-072-25  
 Alignment Scores:  
 Pred. No.: 1,02e-250 Length: 3544  
 Score: 2606.00 Matches: 516  
 Percent Similarity: 90.21% Conservative: 0  
 Best Local Similarity: 90.21% Mismatches: 1  
 Query Match: 97.68% Indels: 56  
 DB: 17 Gaps: 1  
 US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)



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; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Alignment Scores:
Pred. No.: 1,02e-250 Length: 3544
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97.68% Indels: 56
DB: 19 Gaps: 1

US-09-964-277-21 (1-517) x US-10-377-072-25 (1-3544)

QY 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db 869 ATGTTGGCTCTCTCTTCTCAGACTGTTTCTCAGCTGTAATCTCTGGGTAAACTGGAGAAGA 928
QY 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 929 GCTTCAACTCTGTTCACTCGCTTGCA-GGTGGGTTTGTGTGAGTTCCTCGTTGTTTCCT 987
QY 29 ----- 29
Db 988 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCT 1047
QY 29 ----- 29
Db 1048 GTTGCCAACTTTGGGCCAACCCGAAATCTTCCCAATCTTTATCTTTGGCTGCCAGCGAGAT 1107
QY 30 -----GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 1108 GTTCCTCAACAAGAGCTGATGAGCAGAAATGGGATTTGGTTATGTTAAATGCCAGCAAT 1167
QY 46 ThrCysProLysProAspPheIleProGluSerHisPheLeuArgValProValAsnAsp 65
Db 1168 ACCTGTCCAAAGCCTGACTTTATCCCGAGTCTCATTTCTCGGTGGCTGTGATGAC 1227
QY 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db 1228 AGCTTTTGTGAGAAAATTTGGCGTGGTGGACAAATCAGTAGATTTTCATTGAGAAGCA 1287
QY 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 1288 AAAGCCTTCAATGGATGTTCTAGTGCACGTGTTAGCTGGGATCTCCCGCTCCGCCACC 1347
QY 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 1348 ATCGTATCGCTACATCATGAGAGATGGACATGTCCTTAGATGAGACTTACAGATT 1407
QY 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 1408 GTGAAAGAAAAAGACCTACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCCTGGAC 1467
QY 146 TyrGluLysLysIleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165

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Db 1468 TATGAGAAAGAGATTAAAGAACCACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTG 1527
QY 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db 1528 CTGCACCTGGAGAAGCAAAATGAACCTGTCCCTGCTCTCAGAGGGTGGACAGAAAAGC 1587
QY 186 GluThrProLeuSerProProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1588 GAGAGCGCCCTCAGTCACCCCTGTGCGGACTCTCTACCTCAGAGGCGAGCAAGG 1647
QY 206 ProValHisProAlaSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1648 CCCGTGCATCCCGCAGCGTCCAGCGTCCAGAGCGTGCAGCCGTCGCTGTTAGAGGAC 1707
QY 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1708 AGCCCGCTGGTACAGGGCGCTCAGTGGGCTGCACCTGTCGAGACAGGCTGGAAGACAGC 1767
QY 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db 1768 AATAAGCTCAAGCGTCTCTTCTCTCGATATCAAAATCAGTTTCATATTCAGCCAGCAATG 1827
QY 266 AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db 1828 GCAGCATCCTTACATGCTTCTCTCATCAGAGATGCTTTGGATATACTACAAACCTTCC 1887
QY 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db 1888 ACTACTCTGGATGGGACCAACAGCTATGTCAGTTCTCCCTGTTTCAGGAATCTATCGGAG 1947
QY 306 GlnThrProGluThrSerProAspLysGluAlaSerIleProLysLysLeuGlnThr 325
Db 1948 CAGACTCCGAAACCACTGCTGATAAGAGAGAAAGCCAGCATCCCCCAAGAACTGCAGACC 2007
QY 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValArgThrSerSerSerGly 345
Db 2008 GCCAGGCTTCAGACAGCCAGAGAGGATGATTCGTTCCGTCAGAACCCAGCAGAGTGC 2067
QY 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db 2068 ACCGCCAGAGGTCCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGCAAAATTAC 2127
QY 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 2128 CACACCAAGTTCCTTTTTCGGCTTTCACACAGCCAGCAGACCTCACGAAAGTCTGCTGGC 2187
QY 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 2188 CTGGGCTTAAAGGCTGGCACTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2247
QY 406 ThrSerSerTrpTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 2248 ACCAGCAGCTGGTATTTTGGCCACAGAGTCTCACACTTCTACTCTGCTCAGCCACTTAC 2307
QY 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 2308 GGAGCGAGTGCAGTTACTCTGCTTACAGCTGCAGCCAGCTGCCACCTTTCGGAGACCAG 2367
QY 446 ValTyrSerValArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db 2368 GTCTATTCTGTCGCGAGCGGCAGAACCAAGTGCAGAGCTGACTCCGCGGAGAGCTGG 2427
QY 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 2428 CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCGAGAAGCTGCCAATGGAATTTGGA 2487
QY 486 GluSerIleMetSerGluAsnArgSerArgGluLeuGlyLysValGlySerGlnSer 505
Db 2488 GAGAGCATCATGTCTCAGAGAACAGGTTCACGGGAAGAGCTGGGGAAGTGGGAGTCACT 2547
QY 506 SerPheSerGlySerMetGluIleGluValSer 517

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Db 2548 AGCTTTTCGGCAGCATGGAAATCATTTGAGGTCTCC 2583
RESULT 15
US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

Alignment Scores:
Pred. No.: 1,066-250 Length: 3625
Score: 2606.00 Matches: 516
Percent Similarity: 90.21% Conservative: 0
Best Local Similarity: 90.21% Mismatches: 1
Query Match: 97,68% Indels: 56
Db: 18 Gaps: 1

US-09-964-277-21 (1-517) x US-10-425-114-26234 (1-3625)

Qy 1 MetLeuProLeuSerLeuGlnThrValPheSerLeuTyrPheTrpValAsnTrpArgArg 20
Db 972 ATGTGTCCTCTCTCTCTCAGACTGTTTCTCAGTACTTCTCAGTACTTCTGGGTAAACTGGAGAAGA 1031

Qy 21 AlaSerThrLeuPheThrCysLeuGln----- 29
Db 1032 GCTTCAACTCTGTTACCTGCTTGCA-GGTGGGTTTGTGCTGAGTCTCTCGTTGTTTCCCT 1090

Qy 29 ----- 29
Db 1091 GGCCTCTGTGAAGAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTTGCTTACCT 1150

Qy 29 ----- 29
Db 1151 GTTGCCCAATTTGGGCAACCGAATCTTCCCAATCTTATCTTGGCTGCCAGCAGAT 1210

Qy 30 ----- GluLeuMetGlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerAsn 45
Db 1211 GTCTCTCAACAGAGCTGTAGCAGCAGAGATGGATTGTTATGTTGTTAAATGCCAGCAAT 1270

Qy 46 ThrCysProLysProAspPheLeuProGluSerHisPheLeuArgValProValAsnAsp 65
Db 1271 ACCTGTCCAAAGCCTGACCTTTATCCCGAGTCTCTATTCTCGCTGTGCTGTAATGAC 1330

Qy 66 SerPheCysGluLysIleLeuProTrpLeuAspLysSerValAspPheIleGluLysAla 85
Db 1331 AGCTTTTGTGAGAAAATTTTGGCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCA 1390

Qy 86 LysAlaSerAsnGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThr 105
Db 1391 AAAGCCTCCNATGGATGTTCTTAGTGCACTGTTTAGCTGGGATCTCCCGCTCCGCCACC 1450

Qy 106 IleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGluAlaTyrArgPhe 125
Db 1451 ATCGCTATCGCTTACATCATGAAGAGCATGGACATGCTTTAGATGAAGCTTACAGATT 1510

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Qy 126 ValLysGluLysArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAsp 145
Db 1511 GTGAAAGAAAAGACCTACTATATCTCCAAATTTCAATTTTCTGGGCAACTCTCTGGAC 1570

Qy 146 TyrGluLysIleLeuAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeu 165
Db 1571 TATGAGAAGAAGATTAGAACCCAGACTGGAGCATCAGGGCCCAAGAGCAAACTCAAGCTG 1630

Qy 166 LeuHisLeuGluLysProAsnGluProValProAlaValSerGluGlyGlyGlnLysSer 185
Db 1631 CTGCACCTGGAGAAGCCAAATGAACCTGCTCTCTCAGAGGGTGGACAGAAAAAGC 1690

Qy 186 GluThrProLeuSerProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArg 205
Db 1691 GAGAGCGCCCTCAGTCCACCTGTCGCCACTCTGCTACCTCAGAGGCGCAGGACAAAGG 1750

Qy 206 ProValHisProAlaSerValProSerValGlnProSerLeuLeuGluAsp 225
Db 1751 CCCGTGTCATCCCGCAGGCTGCCAGCTGCCAGCTGCCAGCTGCCAGCTGCCAGGAC 1810

Qy 226 SerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSer 245
Db 1811 AGCCCGCTGTACAGGCGCTCAGTGGGCTGCACCTGTCGCGCAGCAGGCTGGAAGACAGC 1870

Qy 246 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrSerAlaSerMet 265
Db 1871 AATAAGCTCAAGCGTTCCTCTCTGATATCAAAATCAGTTCTATATTCAGCCAGCATG 1930

Qy 266 AlaAlaSerLeuHisGlyPheSerSerGluAspAlaLeuGluTyrTyrLysProSer 285
Db 1931 GCAGCATCCTTACATGGCTTCTCTCATCAGAAGATGCTTTGGAAATACTACAACTTCC 1990

Qy 286 ThrThrLeuAspGlyThrAsnLysLeuCysGlnPheSerProValGlnGluLeuSerGlu 305
Db 1991 ACTACTCTGGATGGACCAACAAGCTATGCCAGTTCCTCCCTGTTTCAGGAACATATCGGAG 2050

Qy 306 GlnThrProGluThrSerProAspLysGluGluAlaSerIleProLysLysLeuGlnThr 325
Db 2051 CAGACTCCCGAAACCAGTCTCTGATAAGGAGGAAGCCAGCATCCCCAAGAAGCTGCAGACC 2110

Qy 326 AlaArgProSerAspSerGlnSerLysArgLeuHisSerValAtqThrSerSerSerGly 345
Db 2111 GCCAGGCTTCAGACAGCCAGCAAGCGATTGCATTCCGTTCAGAACCCAGCAGCAGTGGC 2170

Qy 346 ThrAlaGlnArgSerLeuLeuSerProLeuHisArgSerGlySerValGluAspAsnTyr 365
Db 2171 ACCGCCCAGAGTCCCTTTTATCTCCACTGATCGAAGTGGAGGCTGGAGGACATTTAC 2230

Qy 366 HisThrSerPheLeuPheGlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGly 385
Db 2231 CACACCAGCTTCCTTTTCGGCCTTTCCACAGCCAGCAGCAGCTTCACGAAGTCTGTGGC 2290

Qy 386 LeuGlyLeuLysGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 405
Db 2291 CTGGGCTTTAAGGGCTGGCCTCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTG 2350

Qy 406 ThrSerSerTyrTyrPheAlaThrGluSerSerHisPheTyrSerAlaSerAlaIleTyr 425
Db 2351 ACCAGACCTGGTATTTTGGCCACAGAGTCTCTCACACTTCTACTCTGCTCAGCATCTAC 2410

Qy 426 GlyGlySerAlaSerTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGln 445
Db 2411 GGAGCAGTGGCAGTCTACTCTGCTTACAGCTGACAGCTGCCACCTTGGGAGACCAA 2470

Qy 446 ValTyrSerValArgArgArgGlnLysProSerAspArgAlaAspSerArgArgSerTrp 465
Db 2471 GTCTATTCTGTGCGCAGGCGGAGCAAGTGTGACAGAGCTGACTCCGCGGAGCTGG 2530

Qy 466 HisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGlnMetGluPheGly 485
Db 2531 CATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACCAGAGCTGCCAATGGAAATTTGA 2590

Qy 486 GluSerIleMetSerGluAsnArgSerArgGluGluLeuGlyLysValGlySerGlnSer 505

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Db 2591 GAGAGCATCATGTCCAGAGAACAGGTACCGGGAAGAGCTGGGGAAGAGTGGGCAGTCAGTCT 2650

Qy 506 SerPheSerGlySerMetGluIleGluValSer 517

Db 2651 AGCTTTTTCGGCAGCATGGAAATCATTTGAGGCTTCC 2686

Search completed: September 1, 2005, 14:43:35  
Job time : 989 secs